

**FIGURE 1**

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTCAGATCTGCTCGGTAGA  
 CCTGGTGCACCACCACC**ATG**TTGGCTGCAAGGCTGGTGTCTCCGGACACTACCTTCTAGG  
 GTTTTCCACCCAGCTTTTCCACCAAGGCCCTCCCTGTGTGAAGAATTCATCACGAAGAATCA  
 ATGGCTGTTAACACCTAGCAGGGGAATATGCCACCAAAACAAGAATTTGGGATCCGGCGTGGGA  
 GAACCTGGCCAAAGAACTCAAAGAGGCAGCATTGGAACCATCGATGGAAAAAATATTTAAAAATT  
 GATCAGATGGGAAGATGGTTTGTGCTGGAGGGGCTGCTGTTGGTCTTGGAGCATTGTGCATA  
 CTATGGCTTGGGACTGCTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCTCAGT  
 ATGTCGAAGGATAGAATTCATCCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACAGCT  
 TTGTCTGCCATAGCAATCAGCAGAACGCCCTGTTCTCATGAACCTTCATGATGAGAGGCTCTTG  
 GGTGACAATTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC  
 CATATGACCAGAGCCAGGCCCAAAGCATCTTGCTTGGTGTCTACATTCTGGTGTGATGGGT  
 GCAGTGGTGGCTCCTCTGACAAATATTAGGGGGTCTCTTCTCATCAGAGCTGCATGGTACAC  
 AGCTGGCATTGTGGGAGGCCCTCCCACTGTGGCCATGTGTGCGCCCACTGAAAAGTTTCTGA  
 ACATGGGTGCACCCCTGGGAGTGGGCCCTGGGTCTCGTCTTGTGTCTCATTTGGGATCTATG  
 TTTCTTCCACCTACCACCGTGGCTGGTGGCACTCTTTACTCAGTGGCAATGTACGGTGGATT  
 AGTTCCTTTTCCAGCATGTTTCCCTTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAGTAT  
 CACCAGTGTATGGAGTTCAAATAATATGATCCCATTAACTCGATGCTGAGTATCTACATGGAT  
 ACATTAATAATATATTTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAGAAA**TG**  
**A**AGTGACTCAGCTTCTGGCTTCTCTGTCTACATCAAATATCTTGTTTAATGGGCGCATATGC  
 ATTAATAAGTTTGTACAAGCAGCTTTCGTTGAAGTTTAGAAGATAAGAAACATGTATCATA  
 TTTAAATGTTCCGGTAATGTGATGCCCTCAGGTCTGCCTTTTTTCTGGAGAATAAATGCAGT  
 AATCCTCTCCCAAATAAGCACACACATTTCAATTCTCATGTTTGAGTGATTTTAAATGTT  
 TTGGTGAATGTGAAAACATAAAGTTTGTGTATGAGAATGTAAGTCTTTTTTCTACTTTAAAA  
 TTTAGTAGGTTCACTGAGTAACATAAATTTAGCAAACTGTGTTTGCATATTTTTTTGGAGT  
 GCAGAATATTGTAATTAATGTATAAGTGATTTGGAGCTTTGGTAAAGGACACAGAGAAG  
 GAGTCACCTGCAGTCTTTTGTGTTTTTAAATACTTAGAACTTAGCACTTGTTTATTGATTA  
 GTGAGGAGCCAGTAAGAAACATCTGGGTATTTGGAACAAGTGGTCATTGTTACATTCATTT  
 GCTGAACCTTAACAAAACGTGTTCACTCCTGAACAGGCACAGGTGATGCATTCTCTGCTGTTG  
 CTCTCAGTGCTCTCTTTCCAAATATAGATGTGGTCATGTTTGACTTGTACAGAAATGTTAATC  
 ATACAGAGAATCCTTGATGGAATATATATGTGTGTTTTACTTTTGAATGTTACAAAAGGAA  
 ATAACCTTTAAACATTTCTCAAGAGAAAATATTCAAAGCATGAAATATGTTGCTTTTCCAG  
 AATACAAACAGTATACTCATG

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MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRGTQGEI  
KEAALEPSMEKIFKIDQMGRWFVAGGAUVGLGALCYGYGLSNEIGAIEKAVIWPQYVKDRI  
HSTYMYLAGSIGLTALSAIAISRTPVLMNFMMRGWSWVTIGVTFAMVGAGMLVRSIPYDQSP  
GPKHLAWLLHSGVMGAVVAPLTLIGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL  
GVGLGLVFVSSSLGSMFLPPTTVAGATLYSVAMYGGLVLFMSMFLLYDTQKVIKRAEVSPMYGV  
QKYDPINSMLSIIYMDTLNIFMRVATMLATGGNRKK

**FIGURE 3**

GAAGGCTGCCTCGCTGGTCCGAATTTCGGTGGCGCCACGTCGCCCGCTCTCCGCTTCTGCAT  
CGCGGCTTCGGCGGCTTCCACTAGACACTAACAGTCGCGGAGCGCGCGCTCGTGAGGG  
GCTCGGCACGGGGAGTCGGGCGGCTTGTGCATCTTGGCTACCTGTGGTCCGAAGATGTCGG  
ACATCGGAGACTGGTTCAGGAGCATCCCGCGCATCAGCGCTATTGGTTTCGCGCGCCACCGTC  
GCCGTGCCCTTGGTCGGCAAACTCGCCCTCATCAGCCCGGCTACTCTTCCCTCTGGCCGGA  
AGCCTTCCCTTATCGCTTTCAGATTTCGGAGGCAATCACTGCCACCTTTTATTTCCCTGTGG  
GTCCAGGAACGTAATTCTTATTTGGTCAATTATATTTCTATATCAGTATTTCTACGGCA  
CTTGAAACACGACTTTTGATGGGAGGCCAGCAGACTATTTATTATGCTCCCTCTTTAACTG  
GATTGCTATCTTATGTCTGGGCCCAGCTGAACAGAGACATGATTGTATCATTTTGGTTTGA  
ACACGATTTAAGGCTGCTATTTACCTGGGTTATCCTTGGATTCAACTATATCATCGGAGG  
CTCGGTAATCAATGAGCTTATTTGGAATCTGGTTGGACATCTTATTTTTCTCAATGTTCA  
GATACCAATGGACTTGGGAGGAAGAAATTTCTATCCACACCTCAGTTTTTGTACCGCTGG  
CTGCCAGTAGGAGAGGAGGATATCAGGATTTGGTGTGCCCCCTGCTAGCATGAGGCGAGC  
TGCTGATCAGAATGGCGGAGGCGGAGACACAACCTGGGCGCAGGGCTTTCGACTTGGAGACC  
AC**TGA**AGGGGCGGCTCTGGCGAGCGCTCCTCTCAAGCCACATTTCTCCAGTGCTGGGTG  
CACTTAAACACTGCGTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTCTTTC  
AGTACGAGACAAAGTTTCTTAAATCCCGAAGAAAAATATAAGTGTTCACAAGTTTACAGAT  
TCTATTCAAGTCTTACTGCTGTGAAGAACAATAACCAATGTGCCAAATGTGCAAACTGAC  
TACATTTTGGTGCTCTTCTCTCTCCCTTTCCGCTCGAATAATGGGTTTACGGGGTCT  
AATCTGCTGGCATTGAGCTGGGGCTGGGTCAACAAACCTTCCCAAAAGGACCTTATCTCTT  
CTTGGCACATGCTCTCTCCCACTTTTCCCAACCCCCACATTTGCAACTAGAAAAAGTTG  
CCCATAAATTTGCTCTGCGCTTGACAGGTTCTGTATTATTATTGACTTTTGCCAAAGGCTGGT  
ACAAATATCATATTACGCTTATTTCCCTTTTGGTGGCAGAACTGTACCAATAGGGGGAG  
AGACAGCCACGGATGAAGCGTTTCTCAGCTTTTGGAAATGCTCGACTGACATCCGTTGT  
AACCGTTTGGCACCTCTCAGATATTTTTATAAAAAAGTACCACCTGAGTTCATGAGGGCCA  
CAGATTGGTTATTAATGAGATACGAGGGTTGGTGCTGGGTGTTTGTTCCTGAGCTAAGTA  
TCAAGACTGTAGTGGAGTTGCACCTAACATGGGTAGGTTTAAACATAGGGGATGCACCC  
TTTGCCTTTCATATGATGCCCTACTGGCTTGTGTAGCTGGAGTGTGGGTTGCTTGTG  
TAGGAGGATCAGATCATGTTGGCTACAGGAGATGCTCTTTGAGAGGTCCTGGGCATTG  
ATTCACATTTCAATCTCATCTGGATATGTGTTTATTGAGTAAAGGAGGAGAGACCCCAT  
CGCTAATTTAAATGTCACTTTTTTGCCTATCCCCGTTTTTGGTCTATGTTTCAATTAAATGT  
GAGGAAGGCGCAGCTCCTCTCTGCACGTAGATCATTTTTTAAAGCTAATGTAAGCATAATTG  
AGGGAATAACATGATTTAAGGTTGAAATGGCTTTAGAATCATTTGGGTTTGGAGGTGTGTTA  
TTTGTAGTCATGAATGTACAAGCTCTGTGAATCAGACCAAGCTTAAATACCCACACTTTTT  
TCGTAGTGGGCTTTCTATCAGAGCTTGGCTCATAACCAATAAAGTTTTTTGAAGGCCA  
TGCTTTTACACAGTTATTTTATTTATGACGTTATCTGAAAGCAGACTGTTAGGAGCAGT  
ATTGAGTGGCTGTCACTTTGAGGCAACTAAAAAGGCTTCAACAGTTTTTGTATCAGTTTCTT  
TTCAGGAACATTTGTCTTAAACAGTATGACTATTCTTCCCCCACTCTTAAACAGTGTGAT  
GTGTGTTATCTTAGGAAATGAGAGTTGGCAACAACTTCTCATTTTGAATAGAGTTTGTGTG  
TACTTCTCCATATTGATTTATATGATAAAATAGGTGGGAGAGTCTGAACCTTATGATGTA  
TGTTTTGTGTTTCATCTGTGGGCCACATAAAGTTTACTTGTAAAAATTTAGAGGCCATTACT  
CCAAATATGTTGTGACGTACCTATTGTACAGGCTGGAGACTCATTGTATGATATAAGAATA  
TTTCTGACAGTGTGAGTACCCGGAGTCTCTGGTGTACCCCTCTTACCCAGTCACTGCTCGC  
CAGTCACTTTTTTCTTAAAGGTTTACAGTATTTAGAACTTTTTCAGTTTCAGGGCAAAATGTT  
ATAAGAGTTTATCTCTTAAACATGGTTAGGAAGCTGTAGCTTATTTGATTTTGTCTGGATT  
ATGTTCTGGAATAATTTTACCAAAACAAAGCTATTTGAGTTTTCAGTTGACAAAGGCCAAAC  
TGACAGTGGATTCTCTTTACAAATGGAATAAAAAATCCTTATTTTGTATTAAGGACTTCC  
TTTTTGTAACTAATCTCTTTTATTGGTAAAAATGTAAATTAAGTGTCAACTTG

**FIGURE 4**

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGGLISPAYLFLWPEAFLYRFQIWRPITATFYF  
PVGPGTGFLYLVLNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP  
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL  
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWQGQFRL  
GDQ

**Transmembrane domain:**

amino acids 98-116, 152-172

**N-myristoylation site.**

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

**Glycosaminoglycan attachment site.**

amino acids 218-222

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTCATTAAGTGGTGT  
GTAGCTTCTATCTCGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCTACTCCCTCTCGGCT  
CCTTGTGGCCAAAGGCTAACCGGGGTCGCGCGGTCTGGCCTAGGGATCTTCCCGTTGCC  
CCTTTGGGCGGGGATGCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG  
CGGGGTTCTGCGAGGCCCAGACTGGTCCATCCCATCTTGGACTTTGTGGAACAGAAATGT  
GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCAGAGCCGCTGATTTTGGT  
GGCCTGTGTTCCCTTGTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATT  
ATCAGGAATACAAAGAACTAGTTGAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAAT  
AATGAAGATCAATTTCAAGAAGCATGCACCTTCTCCTCTTGCAAAGACCCATACATCACAGG  
CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTACTATCTTTAAAGCAATGATGGTCCAGA  
AAAACATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAAGAGAGAAATGGTGTATTACCT  
GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAATCCT  
GAGGGAAGTCTTAGAAAATCAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAA  
AACAGTTATCAGAGGCTAAAAAGAGAGCCACAGTGCATTCCAGTGAAGTGAATTAATG  
AATAATTCCTCAAGGGGATGGTGAACATTTTGACACCCACCCCTCAGAAGTTAAATGCTATT  
TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGGAAGGTCTGAAACTTCCTCCCTCC  
CACAAAAGGCGCTGAAGATTCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAA  
TTATCAGTACTTGGAAACAGAAGAACTTCGGCAACGAGAACACATATCTCAAGCAGAAGAGAG  
TAAGTTCAGTGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG  
GAAAACCCATGCGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAG  
CAAACATTACTAAAGAGGAGATTGCTTCGAGAGAAACTCAAAGAAGAGTTATTAATAAGTA  
ATAATTAAGAACAAATTTAACAAATGGAAGTTCAAATTGTCTTAAAAATAAATTATTTAGTC  
CTTACACTG

**FIGURE 6**

MAAEEDEVEWVVESIAGFLRGPDWSIPILDFVEQKCEVNCKGGHVITPGSPEPVILVACVP  
 LVFDDEESKLTYTEIHQYKELVEKLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP  
 VLAEDFTIFKAMMVQKN IEMQLQAIRIIQERNGLVPDCLTDGSDVVSDLEHEEMKILREVL  
 RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS  
 IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS  
 MRKDMRTKQIQNMEQKKGKPTGEVEEMTEKPEMTAEKQTLLKRLLAEKLKEEVINK

**N-glycosylation sites.**

amino acids 224-228, 246-250, 285-289

**N-myristoylation site.**

amino acids 273-279

**Amidation site.**

amino acids 252-256

**Cytosolic fatty-acid binding proteins.**

amino acids 78-108

**FIGURE 7**

GGGCACAGCACATGTGAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT  
TCATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA  
TTAATGAAGATCAATTTCAAGAAGCATGCACCTTCTCCTCTTGCAAAGACCCATACATCACAG  
GCCATTTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC  
AGAAAAACATTGAAATGCAGCTGCAAGCCATTCTGAATAATTCAAGAGAGAAATGGTGTATTA  
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAT  
CCTGAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAA

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**FIGURE 8**

GCGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTG  
 TAGCTTCTCCACGTATGGACCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG  
 TCTCAGCTCTAGGATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATAAAAAAC  
 AGTGGGAATGGAAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCAACAATGTATAC  
 ATTCTGCTAGGTGCCATATTATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATT  
 CTGCCAATGAAGAAAACAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAAGT  
 GTGAAGCTAGTTTTCTGTGTGCTTGTGCATTTCTGTGTATATAAGAAAGATCATCAAAGTAG  
 AAATTTGAAATATGCTTCTGGAAGGAATCTCTGATTTTCATGAAGTGGTCCATTCTGCCT  
 TTCTTTATTTCTCGGATAAATTGATTGCTTCTATGTCCTGCTCTATCTTCAACGACCATG  
 GCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTTCTATTACAGGATAGTGCTGAA  
 GAGGCGTCTAAACTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCT  
 TGACTGCCGGGACTAAACCTTTACAGCACAACTTGGCAGGACGTGGATTTCATCACCATGCC  
 TTTTTCAGCCCTTCCAATTCCTGCCTTCTTTTCAAGAGTGAAGTGTCCAGAAAAGACAATTG  
 TACAGCAAAAGGAATGGACTTTTCTGAGCTAAATGGAACACCACAGCCAGAGTTTTCAGTC  
 ACATCCGCTCTTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTTTTATTCTTCAATGGCT  
 AATATCTATAATGAAAGATACTGAAGGAGGGGAACAGCTCATGAAAGCATCTTTCATACA  
 GAACAGCAAACTATTCTTTTGGCATTCTGTTTAAAGGGCTGACTCTGGGCCCTCAGAGGA  
 GTAACCGTGATCAGATTAAGAAGTGTGGATTTTTTTATGGCCACAGTGCATTTTCAGTAGCC  
 CTTATTTTGAAGTGCATTCAGGGGCTTTTCAGTGGCTTTTCATTCTGAAGTTCCTGGATAA  
 CATGTTCCAGTCTTTGATGGGCCAGGTACCACGTGCATTTATCAACAAGTGTCTGTCCCTGG  
 TCTTTGACTTCAGGCCCTCCCTGGAATTTTCTTGGAGCCCATCAGTCTTCTCTCTATA  
 TTTATTTATAATGCCAGCAAGCCTCAAGTTCGGGAATACGCACCTAGGCAAGAAAGGATCCG  
 AGATCTAAGTGGCAATCTTTGGGAGCGTTCCAGTGGGGATGGAGAAGAACTAGAAAAGCTTA  
 CCAAACCCAAGAGTGATGAGTCAGATGAAGATACTTTCTAACTGGTACCCACATAGTTTGA  
 GCTCTCTGAACCTTATTTTTCACATTTTCAGTGTTTGAATATTTATCTTTTCACTTTGATA  
 AACCAGAAATGTTTCTAAATCCTAATATTCTTGCATATATCTAGCTACTCCCTAAATGGTT  
 CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATCTAAAGAAGTATACAGGAGTAACA  
 ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT  
 TTTCTTGGCCTTCAAGCTTCCAAAAAAGCTTGTAAATATCATGTTAGTATAGCTTGTATAT  
 ACACATAGAGATCAATTTGCCAAATATTACAATCATGTAGTTCTAGTTTACATGCCAAAGT  
 CTCCCTTTTAAACATTATAAAGCTAGGTGTCTCTTGAATTTTGGGCCCTAGAGATAGT  
 CATTTTGAAGTAAAGAGCAACGGGACCCCTTTCTAAAGAGCTTGGTTGAAGGACCTAAATAC  
 CTGGCCATACCATAGATTGGGATGATGTAGTCTGTGCTAAATATTTTGTCTGAAGAAGCAGT  
 TTCTCAGACACAACATCTCAGAATTTAATTTTTAGAAATTCATGGGAATTTGGATTTTTGT  
 AATAATCTTTTGTATTTTAAACATTTGGTTCCTAGTCACCATAGTTACCACTTGTATTTTA  
 AGTCATTTTAAACAAGCCAGGTGGGGCTTTTTCTCCTCAGTTTGAAGGAGAAAATCTTGAT  
 GTCAATCTCCTGAATTTATACATTTTGGAGAATAAGAGGGCATTTTATTTTATAGTTAT  
 AATTCAAGCTGTGACTATTGTATATCTTTCCAAGAGTTGAATGCTGGCTTCAGATCATAC  
 CAGATTGTGCTGAGGATGATGCTTAGGAACCTTTAAAGGGATCCTTCAAAGGATCACTT  
 AGCAAAACACATGTTGACTTTTAACTGATGTATGAATATTAATCTCTAAAAATAGAAAGACC  
 AGTAATATATAAGTCACTTTACAGTGCTACTTCAACCTTAAAGATGCATGGTATTTTGTG  
 GTATTTTGCATCGAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTAA  
 AAATTAGCAAAACAAAGTGACTTGTCTAGGGTTCATCGAGCTGGGTGATGATAGAAGAGTGGG  
 CTTTAACTGGCAGGCTGTATGTTTACAGTACCATACCTGTAATATGAGCTTATGGTGT  
 CATTCTCAGAACTTATACATTTCTGCTCTCCTTTCTCCTAAGTTTCATGCAGATGAATATA  
 AGGTAATATACTATTATATAATTCATTGTGATATCCCAATAATATGACTGGCAAGAATTG  
 GTGGAATTTGTAATTAATAATTTATTAACCT



**FIGURE 9**

MEKQCCSHPVICSLSIMYTFLLGAIFIALSSRRILLVKYSANEENKYDYLPTTVNCSELVK  
LVFCVLVSFCVIKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFVYLSYLQPAMAV  
IFSNSFIITALLFRIVLKRRLNWIQWASLLTFLSIVALTAGTKTLQHNLAGRGFHHDAFF  
SPSNSCLLFRSECPKRDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFTSSMANI  
YNEKILKEGNQLTESIFIQNSKLYFFGILFNLTLGLQSRNRDQIKNCGFFYGHSAFSAVALI  
FVTAPQGLSVAFILFDLNMHFLVMAQVTTIITVLSVLDVFRPSLEFFLEAPSVLLSIFI  
YNASKPOVPEYAPROERIRDLSGNLWERSGGDGEELERTPKPSDESDEDTF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,  
298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

**FIGURE 10**

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG  
TTCTGCAATAGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC  
GTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG  
GATGTGCGTTCTTCCACTAGAAAGCTCTTCTGAGGGAGGTAATTAACAAACAGTGGAATGGAA  
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCAACAATGTATACATTCTGCTAGG  
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG  
AAAACAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT  
TTCTGTGTGCTTGTGTCAATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA  
TGCTTCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCTGCCITTTCTTTATTTCC  
TGGATAACTTGATTGTCTTCTATGTCTGTCTTCTTCAACCAGCCATGGCTGTTATCTTC  
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTAGGATAGTGCTGAAGAGGCGTCTAAA  
CTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCTTGACTGCCGGGA  
CTAAACTTTA

**FIGURE 11**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGCCGGCTTGCGTAGCGCGGGCGGCC  
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCTGCGGGGCGAGAGGAGCAT  
 CCCGCTACAGGTTCCCAAGCGGCGTGGCCCGCGGGTTCATGGCCAAAGGAGAAGGCGCCGAG  
 AGCGGCTCCGCGGCGGGGCTGTACCCACCAGCATCCTCCAAAGCACTGAACGCCCGGCCCA  
 GGTGAAGAAAGAACCGAAAAAGAAACAACAGTTGTCTGTTTGCAACAAGCTTTGCTATG  
 CACTTGGGGGAGCCCCCTACAGGTGACGGGCTGTGCCCTGGGTTTCTTCCTTCAGATCTAC  
 CTATTGGATGTGGCTCAGGTGGGCCCTTTCTCTGCCTCCATCATCTGTTTGTGGGCGGAGC  
 CTGGGATGCCATCAGACCCCTGGTGGGCTCTGCATCAGCAATCCCCCTGGACCTGCC  
 TGGGTCGCCCTTATGCCCTGGATCATCTTCTCCAGCCCTGGCCGTGCTGCTACTTCTCT  
 ATCTGGTTGCTGCCGACTTCCACACGGCCAGACCTATTGGTACCTGCTTTTCTATTGCCT  
 CTTTGAACAATGGTCAGTGTTTCCATGTTCCCTACTCGGCTCTACCATTGTTTCATCAGCA  
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTGCTGGGCAC  
 AGTGCTGGGCACGGCGATCCAGGGACAATCGTGGGCCAAGCAGACACGCCTTGTTCAGG  
 ACTTCAATAGCTCTACAGTAGCTTCAACAAGTGCCAACCATACACATGGCACCCTTCACAC  
 AGGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGTCATTGTCTGTATCTATATAATCTG  
 TGCTGTCTATCTGATCCTGGGCGTGGCGGAGCAGAGAGAACCCTATGAAGCCAGCAGTCTG  
 AGCCAATCGCCTACTTCCGGGGCCTACGGCTGGTTCATGAGCCACGGCCCATACATCAAACTT  
 ATTACTGGCTTCTCTTCACTTCCTTGGCTTTTCTATGCTGGTGGAGGGGAACCTTTGCTCTGTT  
 TTGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCT  
 CGGCCACTTTAAACATTCCCATCTGGCAGTGTTTCTTGACCCGTTTGGCAAGAAGACAGCT  
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA  
 CCTCATCATATACATATGGGCTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTAC  
 TACCCCTGGTCCATGCTGCCTGATGTCTATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT  
 GGAACCGAGCCCATCTTCTTCTCTTCTATGTCTTCTTCAACCAAGTTTGCTCTGGAGTGTC  
 ACTGGGCATTTCTACCTCAGTCTGGACTTTGACGGGTACAGACCCGTGGCTGCTCGCAGC  
 CGGAACGTGTCAAGTTTACACTGAACATGCTCGTGACCATGGCTCCCATAGTTCTCATCTCTG  
 CTGGGCTGCTGCTCTTCAAAATGTACCCCATTTGATGAGGAGAGGCGGCGGAGAAAGAA  
 GGCCTGCAAGCACTGAGGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG  
 AGCTGGCTAGCATCTCTAGGGGCCGCCAGTTGCCGAAGCCACCATGCAGAAGGCCACAG  
 AAGGGATCAGGACCTGTCTGCCGGCTTGCTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA  
 CTGAAGACTCAAGGAGGTGGCCAGGACACTTGCTGTGCTCACTGTGGGGCCGGCTGCTCTG  
 TGGCCTCCTGCTCCCTCTGCTGCTGTGGGGCCAAAGCCCTGGGGCTGCCACTGTGAATA  
 TGCCAAGGACTGATCGGGCTAGCCGGAACACTAATGTAGAAACCTTTTTTTACAGAGCC  
 TAATTAATACTTAATGACTGTGTACATAGCAATGTGTGTATGTATATGTCTGTGAGCTA  
 TTAATGTTATTAATTTTCATAAAGCTGGAAGC

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**FIGURE 12**

MWLRWALS LPPSSCLWAE PGMPSQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSG  
SCPTSH TARPIGTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL  
GTAIQQQIVGQADTPCFQDFNSSTVASQSANHTHGTTSHRETQKAYLLAAGVIVCIYIIICAV  
ILILGVREQREP YEAQQSEPIAYFRGLRLVM SHGPYIKLITGFLTSLAFMLVEGNFVLFCT  
YTLGFRNEFQNL LLAIMLSATLTIPWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI  
ITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVEFTKFASGVSLG  
ISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMYPIDEERRRQNKAL  
QALRDEASSSGCSETDSTELASIL

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**FIGURE 13**

GGGAAACGCAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT  
GCTGTTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA  
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA  
TACTGGCTTCCTTTCACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTGTCTTGTTT  
TGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCTC  
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG  
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC  
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT  
ACCTTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG  
GAACCGAGCCCAT

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**FIGURE 14**

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTACAAAAGGTGCAGGT  
ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAAAACAGAAAACCTGTTAGAAATGT  
GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT  
TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT  
CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG  
CAGTTTTATGCATTGCTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA  
GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGTAAGTGAATACTGAGTTGTTTAGG  
ACTTTCTATTGTGGCAAACCTCCAGAAAAACAACCCCTTTTGCTGCACATGTAAGTGGAGCTG  
TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTTCAGACCATCCTTTCCTACCAAATG  
CAGCCCAAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG  
AGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTTCAGACAGTGGCAATTTTGGGACTG  
ATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT  
ACTGCAGCAGAATGGTCTATGTCATTTTCCTTCCTTGTTTTTCCTGACTTACATTTCGTGA  
TTTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAACCCCTCATGACACTG  
CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCAGAGATATTGATGAAAGGAT  
AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAAGTTGCTTA  
TTCTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA  
ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATCTTAAAGGATATCATCAAGAAGACTA  
TTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAAATAAGTCAAAAGACTATG

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MWWFQQGLSFLPSALVIWTSAAFIIFYITAVTLHHIDPALFYISDTGTVAPEKCLFGAMLNI  
AAVLICIAITYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLEAAHVSG  
AVLTFGMGSLYMFVQTTILSYQMOPKIHGKQVFWIRLLVWICGVSALSMLTCSSVLHSGNFG  
TDLEQLKHNWNPDEKGYVLHMITAAEWSMSFSFSGFFLTYYIRDFQKILSRVEANLHGLTLYD  
TAPCPINNERNTRLSRDI

**FIGURE 16**

CGGACGCTTGGGCNGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT  
TCCGTCTCTCGGGTCTTTTCCTGGTCCCAGGCCAAAGCGGAGCGGAGATCCTCAAACGGCCTA  
GTGCTTCGCGCTTCCGGAGAAAAATCAGCGGTCTAATTAATTCCTCTGGTTTGTGAAGCAGT  
TACCAAGAATCTTCAACCCTTTCCACAAAAGCTAATTGAGTACACGTTCTGTGAGTACA  
CGTTCCTGTTGATTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA  
GTTGTAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT  
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT  
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

CGGACGCTTGGGCNGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT



**FIGURE 17**

CCCACGCGTCCGCCCCGCCGTGCGTCCCGAGTGCAAGTGAGCTTCTCGGCTGCCCGCGGG  
 CCGGGGTGCGGAGCCGACATGCGCCCCGCTTCTCGGCCTCCTTCTGGTCTTCGCGGCTGCAC  
 CTTCCGCTTGTACTTGCTGTGACGCGACTGCCCCGCGGGCGGAGACTGGGCTCCACCGAGG  
 AGGCTGGAGGCAGGTGCTGTGGTTCCCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG  
 GTCCTTCGAGAGTACCGGAAGGAGACCCAGGCCTACGTGTTCTGCTCTTCTCGCGGCGCTA  
 CCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCTCTGAATGTTTTAGCTGGTGCTT  
 TGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTTGACCTCGGTGGGTGCCACATGC  
 TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCCTGATAAAGT  
 GGCCCTGCTGCAGAGAAAGTGGAGGAGAACAGAAACAGCTTGTTTTTTTTCTTATGTTTT  
 TGAGACTTTTCCCATGACACCAAACCTGGTTCCTGAACCTCTCGGCCCCAATTCTGAACATT  
 CCCATCGTGAGTTCTTCTTCTCAGTTCTTATCGGTTTGATCCCATATAAATTCATCTGTGT  
 GCAGACAGGTCATCTGTCAACCTTAACCTCTCTGGATGCTCTTTTCTCTGGGACACTG  
 TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATTCGGAAACCCCATTAATAAATTT  
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACAGTAGAAAAGA  
 CACATGACTCGGATTTTCTGTTTGCCACATCCCTGGACTCAGTTGCTTATTTGTGTAATGGA  
 TGTGGTCCTTAAGCCCCCTCATTGTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG  
 CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGGT  
 TTTCAAACAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAAATGCTGTTGT  
 GGCCGGGCGCGGTGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCCGGTGATTC  
 ACAAGGTCAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAAATCCTGTCTCTAATAAAAAAT  
 ACAAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCAGCTACTCGGGAGGCTGAGGC  
 AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGATCACACCACTGCACT  
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

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**FIGURE 18**

MRPLLGLLLVFAGCTFALYLLSTRLPRGRLGSTEEAGGRSLWFPSDLAELRESEVLREYR  
KEHQAYVFLFLFCGAYLYKQGFAIPGSSFLNVLAGALFGPWLGLLCCVLTSGVATCCYLLSS  
IFGKQLVVSYFPDKVALLQRKVEENRNSLFFFLFLRLFPMTPNWFLNLSAPILNIPVQFF  
FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKFKFSQKHLQ  
LNETSTANHIHSRKDT

**Important features:****Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 101-123, 189-211

**N-glycosylation sites.**

amino acids 172-176, 250-254

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 240-244, 261-265

**N-myristoylation site.**

amino acids 13-19, 104-110, 115-121, 204-210

**Amidation site.**

amino acids 27-31

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 4-15

**Protein splicing proteins.**

amino acids 25-31

**Sugar transport proteins.**

amino acids 162-172

**FIGURE 19**

CCGAGGCGGGAGGAGCCCGAGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTT  
 CCAGTTCTCAGCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAACAGCTCAGAA  
 TAGGAAAATAACTTGGGATTTTATATTGGAAGACATGGGATCTTGCTGCCAACGAGATCAGCA  
 TTTATGACAACTTTCAGAGACTGTTGATTGGTGAGACAGACCGCCATCAGTGTGGCATG  
 TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACC  
 CCCCCGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT  
 TGCTCACTGCCTACTTTGTGATTCAACCTTTCAGCCATTAGCACCTGAGCCAGTGCCTTCT  
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAA  
 GAAGTACATGTCAGAAAATAAGGGAGTTCTCTGCATGGGGTGATGAAGACAGACCCCTTTC  
 CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTGCC  
 AACTGCACTGGCTGTGCCAGAAACACCTGAAGTGATGCTCCTGGAAGACGCCCCAAGGAA  
 ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCTGTTGGAGGAAGAGATTC  
 AGCATTTTTTGTGCCAGTACCCTGAGGCGACAGAAGGCTTCTGTAAGGGTTTTTCGCCAAG  
 TGGTGGCGCTGCTTTCTGAGCGGTGGTCCCATTCTCTATCCATGGAGGAGACCTCTGAA  
 CAGATCACAAATGTTACGTGAGCTTTTCTCTGTTTCACTCACCTGCCATTTCCAAAAGATG  
 CCTCTTTAAACAAGTGCTCCTTTCTTACCAGAACCTGTTGTGGGGAGTAAGATGCATAAG  
 ATGCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA  
 GTGCCGAAGACATTGTGAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTGG  
 ACACCAACCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT  
 GGAACCGCTTTCTCAGAAGCTGTAGGAAATAGAACTGTGCACAGGAACAGCTTCAGAGCCGA  
 AAACCAGGTTGAAAGGGGAAAAATAAAAAACAAAACGATGAAACTGCAAAA

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**FIGURE 20**

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIHQLEKNEPQRPPPYPLLIIVVY  
KVLATLGLILLTAYFVIQPFSPLAPEFVLSGAHTWRSIIHHIRLMSLPIAKKYMSENKGVPL  
HGGDEDRPFPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKT  
GKPLLEEEIQHFLCQYPEATEGFSEGFFAKWWRCFPERWFFPYPWRRPLNRSQMLRELFV  
FTHLPFFKASLNKCSFLHPEPVVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRRHCSVAMP  
IEPGDIGYVDTHWKVYVIARGVQPLVICDGTAFSEL

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CCACGGTGTCCGTTCTTCGCCCGCGCGCAGCTGTCCCGAGGCGGGAGGAGCCGAGGGGCG  
CGAGCCCCGCATGAATCATTTGTAGTCAATCATTTTCCAGTTCTCAGCCGTTCAAGTTGTGATC  
AAGGGACACGTGGTTTTCCGAAGTCCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT  
GGAAGACATGGATCTTGTCTGCCAACGAGATCAGCATTTATGACAAACTTTCAGAGACTGTTG  
ATTTGGTGAGACAGACCGCCATCAGTGTGGCATGTGAGAGAAGGCAATTGAAAAATTTATC  
AGACAGCTGCTGGAAGAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT  
TGTGTATAAGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC  
CTTTAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

**FIGURE 22**

CCCACGCGTCCGCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG  
 CAGGGTCCCCACTTGCAGCTGCAGCAGCTGCAGAGCGCTGCTCCTGGGTGGT  
 CCATGGTGGCAGCGTCTAGACCGTGCTATGAGCGCTGGGGCTGCAGTGGGGACTGCC  
 CTCCTTCCACCCACCAATGGCAGCCCCACTTCTTTGAAGACTTCCAGGCTTTTTGTGCCA  
 CACCCGAATGGCGCACTTTCATCGACAAACAGGTACAGCCAACTGATCCAGATTGCAAAATG  
 GACACGCTTGTGAAGAGCCAGCACTTATGTCAGGTTTCTGGAATGCCTGCTATGACATGCT  
 TATAGCAGTGGCAGCGCGCCAGTGGGAGCGCGCCAGAGTCGTGGGCGCTTCCAGGAGC  
 TGGTGTGGAACCTGCCGAGAGGCGGGCGCGCTGGAGGGGCTACGCTACACGGCAGTGCTG  
 AAGCAGCAGGCAACGCAGCACTCCATGGCCCTGCTGCACCTGGGGGGCGCTGTGGCGGAGCT  
 CGCCAGCCATGTGGGGCTGGGCGCTGAGGGCACTCCCATCCCCCGCTGGAACATGTCCA  
 GCGCCGAGACATATTACGCATGCGTCTGAAGCTGGTGCCCAACCATCACTTCGACCCTCAC  
 CTGGAAGCCAGCGCTCTCCGAGACAACTCTGGGTGAGGTTCCCTTGACACCCACGAGGAGGC  
 CTCACTGCTTCTGGCAGTGACCAAGAGGCCAAAGTGAGCACCCACCGAGTTGCTGCAGG  
 AGGACCACTGCGGCGAGGACGAGCTGGCTGAGCTGGAGACCCGATGGAGGCGAGCAAACTG  
 GATGAGCAGCGTGAGAAGCTGGTGCTGTGGCCGAGTGCCAGCTGGTGACGGTAGTGGCCGT  
 GGTCCCAGGGCTGCTGGAGGTCAACACACAGAATGTATACTTCTACGATGGCAGCACTGAGC  
 GCGTGGAAACCGAGGAGGGCATCGGTATGATTTCCGGCGCCCACTGGCCAGCTGCGTGAG  
 GTCCACTTGGCGGCTTTCAACTGCGCCGTTCAGCACTTGAGCTTCTTTATCGATCAGGC  
 CAACTTCTCTCAACTTCCATGCAAGGTGGGCAGCACCCAGCTCATCTCTACAGCCAGA  
 CTCGAGACCCAGCTGGCCCCATCCCAACCCATACCCAGGTACGGAACCAAGGTGATCTG  
 TGGCTCTGCGCCTACGGCCCTCTCAAGGCTACCTAAGCAGCTCGTGGAGGAGAAGT  
 GCTGCGTGGCTCAGGCCCTTACCCAGAAATGGGTACAGCGTGAGATATCCAACCTCGAGTACT  
 TGATGCACTCAACCACTTGGGGGCGGACCTACAATGACCTGTCTCAGTACCTGTGTTCT  
 CCTGGTCTCTGCAGGACTACGTGTCCCCAACCTGGACCTCAGCAACCCAGCGCTGTCCG  
 GGAAGCTTGAAGCGCTCGGTGTGGTGAACCCCAAGAGCTGCGGAGCTCGTGGAGGAGAAGT  
 ATGAAAGCTTGAGGACCCAGCAGGAGCACTTGACAAGTTCCACTATGGCAACCCACTACTCC  
 AAGCGCAGCGGCGTGTGCACTACCTCATCGCGGTGGAGCCCTCACTCCCTGCACTGCCA  
 GCTGCAAGTGGCGCTTGGACTGCTCCGACCGGCACTTCCACTCGGTGGCGGAGCTGGC  
 AGCGATGTGGTGCTACCCCTGGTGGGCGAGCTCTCCTGAGGACTCATCCAGCAGCACCGCC  
 AGGCTCTGGAGTCCGAGTATGTGTCTGCACACCTACACGAGTGGATCGACCTCATCTTTGCG  
 TACAAGCAGCGGGGGCCAGCCCGGAGGAGGCCCTCAATGTCTTATTACTGACCTATGA  
 GGGGGCTGTAGACTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATT  
 TCAGCAACTTTGGGCAGACTCCCTGTGAGTGTGTAAGGAGCACTCAACTCCTGGCTCTCA  
 GCTGGAGGAAGCAGCCCATCGCCTTGACGCTGGACACTAATCACTCAGCTATCTCCAGCA  
 CTTGGAGCAACTCAAGGCATCTTCGACAGGTTGACTGTGAGTGCCAGTGGGCTGCTGGGCA  
 CCCACAGCTGGTGTGCCATGACCGCAACATAAGCACTACTTCACTTCAGCAAGAGACCCC  
 ACCATGGGCGGCCAACAGCAGCAGCACTGCTGAGTGCCCGTGGGTGCCAGGCACTGGTGT  
 GAGTGGACAAGCACTGGCAGTGGCCCCGATGGAAGCTGCTATTCAAGCGGTGGCCACTGGG  
 ATGGCAGCCTGGGGTGACTGCACTACCCCGTGGAAGCTGTTGAGCCAGCTCAGCTGCCAC  
 CTTGATGTAGTAACCTGCCCTGCACTGGACCACTGTGGCATCTACCTCATCTCAGGCTGCCG  
 GGACACCACTGTCAGTGGTGTGGCGGCTCTGTCATCAGGTTGGTCTGTCAGTAGGCGCTGGC  
 CAAAGCTGTGCGAGTCTGTATGGGCATGGGGCTGCAGTGAGCTGTGTGGCCATCAGCACT  
 GAACTTGATGGCTGTGTCTGGATCTGAGGATGGAACCTGTATACACACTGTAGCCCG  
 CGGACAGTTTGTAGGGGCACTACGGCTCTGGGTGCCACATTCCTGGACCTATTTTCCACC  
 TGGCATTTGGGCTCGAAGGCCAGATTGGTATCAGAGCTCAGCGTGGGAACGTTCTTGGCCG  
 CAGGTCACTTCTCTGCACTGTATTGAGTCAATGGGAAGTTGCGGGCTTCACTGCCCCCT  
 GGCAGAGCAGCACTACAGCCCTGACGGTGACAGAGGACTTTGTGTTGCTGGGCAACCGCCAGT  
 GCGCCCTGACATCTCCAACATAACACACTGCTCCGCGCCCGCTCCCTTGCCCATGGAAG  
 GTGGCCATCCGACAGGTGGCGGTGACCAAGGAGCGCAGCCAGTGGTGGTGGGCTGGAGGA  
 TGGCAAGCTCATCTGGTGGTGGCGGGGAGCCCTCTGAGGTGGCAGCAGCAAGTTCGCGC  
 GGAAGCTGTGGCGGTTCCTGCGGCGCATCTCCAGGTTCTCTGGGAGAGACGGAATAACAAC  
 CCTACTGAGGCGCGCTGAACCTGGCCAGTCCGGTGTCTGGGCGCCGCGCCCGGAGGCGCTG  
 GCCCGGAGAGCCCGCGAGAAGTGGCGGGGAACCCCGGGGTGGGCAACCCAGGCGGTGA  
 GCGGGGCCACCTGCCAGCTCAGGGATTGGCGGGCATGTTACCCCTCAGGGATTGGCG  
 GCGGGAAGTCCCGCCCTCGCGGCTGAGGGGCGCCCTGAGGGCCAGCACTGGCGTCT

**FIGURE 23**

MSQFEMDTYAKSHDLMMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL  
 RYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRKLKLVN  
 HHFDPHLEASALRDLNLEGEVPLTPTEEASLPLAVTKEAKVSTPPPELLQEDQLGEDELALELTP  
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGGSTERVETEEGIGYDFRRP  
 LAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQPGPIPHPTQV  
 RNQVYSWLLRLRPSPQGYLSSRPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRTYNDL  
 SQYPVFPWVLQDYVSPDLDSNPAVFRDLSPKIGVVNPKHAQLVREKYESFEDPAGTIDKFH  
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAAWQARLESADVKELIP  
 EFFFYFPDFLENQNGFDLGLCLQLTNEKVGDVVLPWASSPEDFIQQHRQALESEYVSAHLHEW  
 IDLIFGYKQRGPAEEALNVFYCYEGAVDLDHVTDERERKALEGIISNFGQTPCQLLKEP  
 HPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF  
 SFSKDPMTGSHKTRQLLSGPPVPGSGVSGQALAVAPDGKLLFSGGHWGDSLRVTALPRGKLL  
 SQLSCHLDVVTCLALDTCGIYILISGRDTCMVWRLHLQGGLSVGLAPKPVQVLYGHGAAS  
 CVAISTELDMAVSGSEDTGVIHTVRRGQFVAALRPLGATFPGPFIHFLALGSEGOIVVQSSA  
 WERPGAQVITYSLHLYSVNGKLRASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA  
 PPLPMKVAIRSVAVTKERSHVLVGLLEDGKLIVVAGQPSEVRSSQFARKLWRSSRRISQVSS  
 GETEYNPTAR

**N-glycosylation site.**

amino acids 677-681

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 985-989

**Tyrosine kinase phosphorylation site.**

amino acids 56-65, 367-376, 543-551

**N-myristoylation site.**

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,  
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,  
 873-879, 912-918, 954-960

**FIGURE 24**

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC  
 CACGGCCACCTTGTGAACCTCCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT  
 CCAAAGGCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCTTGGGGCTCTTC  
 TGGACCTTAACTGGGTACTGGCCCTGGGCGCAATGCGTCCTCGCTGGAGCCTTTGCCTCCTT  
 CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCTTAAATCTCTGCCTTCATCC  
 GCACACTCCGTTACCACACTGGGTCAATTGGCATTGGAGCCCTCATCCTGACCCTTGTGCAG  
 ATAGCCCGGGTCATCTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCCTGTAGC  
 CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCTCTGGTGTCTGGAATAATTTATCAAGTTCC  
 TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA  
 AATGCGTTCATGCTACTCATGCGAAACATTGTGAGGGTGGTGTCTGGACAAAGTACAGA  
 CCTGTGCTGTTCTTTGGGAAGCTGCTGGTGGTGGAGGCGTGGGGGTCTGTCTTCTTTT  
 TTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC  
 TGGCTGCCCATCATGACCTCCATCCTGGGGGCTATGTCATCGCCAGCGGCTTCTTACGCGT  
 TTTCGGCATGTGTGGACACGCTCTTCTCTGCTTCTTGGGAAGACCTGGAGCGGAACAACG  
 GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC  
 GAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGAAGCAGCTCCGGCCCTGATCCAGGACTGC  
 ACCCCACCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT  
 AAAAAAAGGTTTTAGGCCAGGCGCGTGGCTCAGCCTGTAATCCAACACTTTGAGAGGCTG  
 AGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCTCC  
 GTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCTATCCAGCTAC  
 TCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGA  
 TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAACAAAAACAAACAA  
 AAAGATTTATTAAAGATATTTTGTAACTC

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**FIGURE 25**

RTRGRTRGGCEKVPINTSCNPHTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGLE  
WTLNWVLALGQCVLAGAFASYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ  
IARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK  
NAFMLLMRNIVRVVLDKVTDLLLFFGKLLVVGVGVLSTFFFSGRIPGLGKDFKSPHLNYY  
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMYSKSLKILGKKN  
EAPPDNKKRKK

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**FIGURE 26**

GAGTCTTTGACCGCCGCCGGGCTCTTGSTACCTCAGCGGAGCGCCAGGCGTCCGGCCGCCGT  
 GGCTATGTTTCGTGTCCGATTTCCGCAAAGAGTTCTACGAGTGGTCCAGAGCCAGAGGGTCC  
 TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTT  
 CAGTGTGACCACGTGCAATATACGCTGGTTCAGTTCCTGGGTGGCAAGAAGTGAAGTGC  
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAAACTGTGGAGCTAATGTAG  
 ACCATTTGGATATTTCTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGG  
 CCAGTCAATGTCGTCAATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA  
 TGACCTTGAAGTTCCCGCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT  
 CAGGAAATGACAGTGTGGGTGAGAGCCTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA  
 GTGGAGCAAACCATGCGGAGGAGGCGCGCGAGAGTGGGAGGCCGAGAGAAGAGACATCCT  
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGTGTTTGTGCTGG  
 CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC  
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGACGCG  
 CCACGTTTCCCGCCACAACCAACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA  
 CACGGATCTCCTTTGAGTATGACCTCCGCTGGTGTCTACACGACTGGTCCCTCCATGAC  
 AGCCTGTGCAACACCAGCTATACCGCAGCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA  
 GCGGCTCCAGGAGTTCCTTGACAGATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTCC  
 AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAATGATTGAAGAGTCTGCAAATAAA  
 TTTGGGATGAAGGACATGCGCGTGCAGACTTTCAGCATTCAATTTGGGTTCAAGCACAAGTT  
 TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT  
 CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG  
 TACCATGGCCTGGAAGTCCGCAAGAAGCAGCTGCGAGGCCACCCAGCAGACCATGCCAGCTGC  
 CTTTGCACCAACCTCGTCATCTCCAGGGGCTTTCTGTACTGCTCTCTCATGGAGGGCAC  
 TCCAGATGTCATGCTGTTCTTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA  
 AGTCTTTGTGTGTTGACAAAGAACCAGGCGCTGCAAACCTGCTGCCCTGGTGTGCTGCC  
 CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC  
 GGACAGGAAGAACTTTTGGGAGGGCGTTTGAAGGCAGCGGAAGCACCAGCTCCCGGA  
 TGCTGCACAACCAATTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT  
 CTGGACGCACCTATTTCCCTCCTGTCTTAGGAATTTGATTCTCCAGAATGACCTTCTTATT  
 TATGTAAGTGGCTTTCAATTTAGATTGTAAGTTATGGACATGATTTGAGATGTAGAAGCCATT  
 TTTTATTAATAAAATGCTTATTTTAGGAAA

**FIGURE 27**

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF  
LEHKEQFHYFILINCGANVDLLDILQPDEDTIFVCDSHRPVNVVNVYNDTQIKLLIKQDDD  
LEVPAYEDIFRDEEEDEEHSGNDSGSEPSEKRTLEEEIVEQTMRRRQRREWEARRRDILF  
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWVAIVGLTDQWVQDKITQMKYVTDVGVLQRH  
VSRHNHRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSLCLNTSYTAARFKLSVHGQKR  
LQEFLLADMGLPLKQVKQKFQAMDISLKENLREMIIESANKFGMKDMRVQTFSIHFGFKHKFL  
ASDVVFATMSLMESPEKDGSGTDHFTQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL  
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKSFVCSTKNRRCKLLPLVMAAP  
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNFHDLVIELKAEDRSKFL  
DALISLLS

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**FIGURE 28**

GTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGTGGCTATGNTCGTGTCCGATTTCCGCA  
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT  
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT  
GGTTCCAGTTTCTGGGTGGCAAGAAGCTTGAAACTGCATTTCTTGAGCATAAAGAACAGTTTC  
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT  
GAAGACACTATATTCTTTGTGTGTGACCCCATAGGCCAGTCAATGTTGTCAATGTATACAA  
CGATACCC

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**FIGURE 29**

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCAGTACCATTATTTTCTAGTGAAC  
 CACGAAGGGACGATACCGAAAAACCCCTCAACCCCAAGGAAATAGACTACAGCCCAATTTG  
 GCTGACTTTGGCTATAGAAAAAGAAAGGAACGAAAAGAGACAGTTTTTTTGGAAAGCTAA  
 GTCTTCCCTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTACAGCTTTTAAACAATT  
 GAGTAAAGTAGCCTCCGGTCACCATGTTGACAGCCCGCTGGGTCCCGTCTGGGCAGCGCTC  
 CTGCTCTTTCTCCTGATGTGTGAGATCCGTATGGTGGAGCTCACCTTTGACAGAGCTGTGGC  
 CAGCGGCTCCGACCGTGTGACTCTGAGGACCCCTGGATCCTGCCCATGTATCTCCTCAG  
 CTCTTCTCCGCGCGCCCGACGCCCTGCCTGAGATCAGACCCCTACATTAATATACCATC  
 CTGAAGGGTGACAAAGGGGACCCAGGCCCAATGGGCCTGCCAGGGTACATGGGCAGGGAGGG  
 TCCCCAAGGGGAGCTGGCCCTCAGGGCAGCAAGGGTGACAAAGGGGAGATGGGCAGCCCCG  
 GCGCCCGCTGCAGAAAGCGCTTCTTCGCCTTCTCAGTGGGCCGCAAGACGGCCCTGCACAGC  
 GCGAGGACTTCCAGACGCTGCTCTTCGAAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGA  
 CATGGCCACCGGCGAGTTTGTGCTGCCCTGCCGTGGCATCTACTTCTTACGCTCAATGTGC  
 ACAGCTTGAATTACAAGGAGACGTACGTGCACATTATGCATAACAGAAAGAGGCTGTCATC  
 CTGTACGCGCAGCCAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTGGC  
 CTACGGGACCCGCTCTGGGTGCGGCTCTTCAAGCCGCGAGCGCGAGAACGCCATCTACAGCA  
 ACGACTTCGACACCTACATCACTTTCAGCGGCCACCTCATCAAGGCCGAGGACGAGTGAAGGG  
 CCTCTGGGCCACCTTCCGCGGTGGAGAGCTCAGGTGCTGGTCCCGTCCCTGCAGGGCTCAG  
 TTGTCACGTCTGTCAGAGCAGGAAGGCCAGGGAGGTCCCGGGGACCTGGCATTCTGGGGAGA  
 CCCTGCTTCTATCTTGGCTGCCATCATCCCTCCAGGCTATTCTGTCTCTCTCTCTCTCTCT  
 TGGACCTATTTTAAAGACTTGTCAACATAAATATTCTAGAATTCTCCGACCTCCGTAGCCC  
 AGCACTTCTCAAACTTGAATAATGCATGCCAATCACCCGGGTTCTGTGTTAAATGCAGATTCT  
 GACTCAGCAGCTCTGAGTGGGTCCAGGATTCTGTGTTCTCATATGTTCTCTGGGTGATCTG  
 ATGGGGTCAGTCTATGAACCACTGGAGCAACCAGGTCTTAGGACTTTCTCAATATTCTAG  
 TACTTTCTGAACATCTTGGAATCTCCACATTTCTAGAAATTCTCCCAACATTTTTTTTGT  
 TGAGACAGACTCTTGCTCTGTGTCAGGCTAGAGTGCAGTGGTGCAATCTCAGTTCACTGC  
 AACCTCTGCTCTCCGGGTTCAAGCGATTCTTCTGCCTCAGCTCCCTGCTGGCTGGGATTAC  
 AGCGGCTGCTACCATGCTGGCTAATTTTTGTATTTTAGTAGAGATGGGGTTTACCATA  
 TTGGCCAGGCTGGTCTTGAACCTCTGACTTCAGGTGACCCACCCGCTCGGCCCTCAAAAT  
 GCTGGGATACAGGTGTGAGCCACCGTGCCTGGCCAATTCCAACATTTCTAAATTTCTCTAT  
 CCTCCAGGGCTCCCGCTGCTATGTTCTCTTTACCCCTTCCCTCTTCTCTTGTCTCAGGCC  
 TGCACCATGCAGCCACCGTTTCAATTTATTCAATTAACACTGAGCACTCACTCTGTGTCT  
 GGTCCCGGGAAGGTTGAGGGGTGAGACACAGGCCCTGCCCTGACCCTCAGTCACTGGCCA  
 GTCACCGCCAGGCGGGGAGAGATGTGTACATAGGTTTTAAAGCAGACCCAGAGCTCTGGGG  
 GCTGTGTTCTGGGTGTTCAAGTGCTGCTGGTCTCCATTACCCACTGCTCCCCAAGGCTGG  
 TGGGACGGGTCGCCGTGTCAGGGGAGGTATCTCCTTCCCGTTCTCTATCCACCTGCCCGAG  
 TGCTCATCTTACAGCAAAACCCAGGGGCTTGGCCAGGTCAAGGGTTCTGTGAGGAGAGG  
 ACCCCAGGAGTGTGGGGGCTATTTGGGGGGTGAAGTGGCCCGGCAAGATGGAACCCACACCCA  
 TAGCTCTCCCAACGCTGATACGGCATCTTGCAGAAAGACCTGACCTCTTCACTGGGATCCC  
 CTCTCTGCTCTCTCCAGGGCTCTGCCAGGGCTTGCTCAGTCCCTTCCACCAAAGTCACTCT  
 GAACCTCCGTTTTCCCGAGGGCTCCAGTCTGCCCTCAGACACTGATGCTCTGTCCCCAGGTGCT  
 CTCTGCCCTCATGCCCCCTCTCACCGGCCAGTGGCCCGACTCTCCAGGCTTTATCAAGGTG  
 CTAAGGCCGGGTGGGCAGCTCTCGTCTCAGAGCCCTCTCCGGCTGGTGTGCTGCTTTAC  
 AAACACCTGCAGGAGAAGGGGCCACGGAAGCCCGAGGCTTTAGAGCCCTCAGCAGGTCTGGGG  
 AGCTAGAGCAAGAGGAGGACCTCAGGCCTTCGTTTCTTCCAGGGTGGGGTGGCCCTGTT  
 GTTCCCTAGCTCTCAAAACCCAGGTGGCTGCCCTCTCTCCCAAGGGGAGGCGGCCCTCCGC  
 CCATTGGTGCTCATGACACTCTGGGGCTGAGGTGCCCGGGGGTGATCTCTGGTGTCTCAC  
 AGCCGAGGGAGCCGTGGCTCCATGGCCAGATGACGGAACAGGGTCTGACCAAGTGCCAGGA  
 AGACTGTGCTATAAACACCCCTGCCCTGATCTTGCCCTGACCCGCGCCAGCCCTGCC  
 GTCCAGCATGATTAAAGAAATGCTGCTCCTCTTGGAAAAAAGAAAAA

**FIGURE 30**

MVTAALGPVWAALLFLLMCEIRMVELTFDRAVASGCQRCCDSEDFLDPAHVSSASSSGRPH  
ALPEIRPYINITILKGDKGDPGMPGLPGYMGREGPQGEPPGPGSGDKGEMGSPGAPCQKRF  
FAFSVGRKTALHSGEDFQTLLFERVFNLDGCFDMATGQFAAPLRGIYFFSLNVHWSWNYKET  
YVHIMHNQKEAVILYAQPSESRIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYIT  
FSGHLIKAEDD

**Important features:****Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 72-75

**Clq domain proteins.**

amino acids 144-178, 78-111 and 84-117

**FIGURE 31**

ACTCGAAGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCGCAGGAAAGACTG  
 AGGCCGCGGCTGCCCGCCCGGCTCCCTGCGCCGCGCGGCTCCCGGGACAGAAAGATG  
 CTCCAGGGTCCCTGCTGCTGCCGTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGCAGG  
 GCTGCCCATCCGGTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCAGTGCAGCGGAGGG  
 ACCACGGTGCCCGAGACGTGCCACCCGACACGGTGGGGCTTACGTCTTTGAGAACGGCAT  
 CACCATGCTCGACGAGGAGCTTTGCCGGCTGCCGGGCTGCAGCTCCTGGACCTGTCA  
 AGAACAGATGCCAGCCTGCCAGCGGGTCTTCCAGCCACTGCCAACCTCAGCAACCTG  
 GACCTGACGGCCAAACAGGCTGCATGAAATCACCATGAGACCTCCGTGGCCTGCGCGCCT  
 CGAGCGCTCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACG  
 TCGACCGCTCCTGGAGCTCAAGCTGCAGGACAACGAGCTGCGGGCACTGCCCGCGCTGCGC  
 CTGCCCCGCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGCAT  
 CCTGGACACTGCCAACGTGGAGCGCTGCGGCTGGCTGCTGCGGGCTGCAGCAGCTGGACG  
 AGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGACAACAGCTGGAG  
 CGAGTGCCACCTGTGATCCGAGGCTCCGGGGCTGACGCGCTGCGGCTGGCCGGCAACAC  
 CCGCATTGCCAGCTGCGGCCGAGGACCTGCGCGGCTGGTGCCTGAGGAGCTGGATG  
 TGAGCAACCTAAGCTGCAAGCCCTGCCTGGCGACCTCTCGGGCTCTTCCCCGCGCTGCGG  
 TCTGCTGGCAGTGCAGCAACCCCTTCAACTGCGTGTGCCCTGAGTGGTGTGGGCCCTG  
 GGTGCGCGAGAGCCAGCTCACACTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCGCCCCA  
 AGAACGCTGGCCGGTGTCTTCTGGAGCTTGACTACGCCGACTTTGGCTGCCAGCCACACC  
 ACCACAGCCAGTGCAGCCACGAGGCGCTGGTGCAGGAGCCCAAGCCTGTCTTCTTAG  
 CTTGGCTCTTACCTGGCTTAGCCCCACAGCGCCGCCACTGAGGCCCCAGCCGCGCTCCA  
 CTGCCCCACCGACTGTAGGGCTGTCCCCAGCCCCAGGACTGCCACCGTCCACTGCCTC  
 AATGGGGGCACATGCCACCTGGGGACACGGCACCACTGGCGTGCTGTGTGCCCGAAGGCTT  
 CACGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACAGTCA  
 CGCCGAGGCCACACGGTCCCTGACCTGGGCATCGAGCCGGTGAGCCCACTCCCTGCGC  
 GTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGCTCACTTA  
 TCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTG  
 AGTACACGGTACCCAGCTGCGGCCCAACGCCACTTACTCCGTCTGTGTATGCCTTTGGGG  
 CCGGGCGGGTGCCGGAGGGCGAGGAGGCTGCGGGGAGGCCATACACCCCCAGCCGCTCCA  
 CTCAACACGCCCCAGTCAACCAGGCCCGCGAGGGCAACCTGCCGCTCTCATTTGCCCGC  
 CCTGGCCGCGGTGCTCCTGGCCGCGTGCTGCGGTGGGGGAGCCTACTGTGTGCGGGCG  
 GGGCGGGCCATGGCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGGCCCT  
 GGAATGGAGGGAGTGAAGGTCCCTTTGGAGCCAGGGCCGAGAGGGGTAGCGCGGTGGAG  
 AGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCAGGGCTGCGCTC  
 CAGTCAACCTCCACGCAAGCCCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCG  
 GGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACACGTAAGTTCTCAGTCC  
 CAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGGCTGTTCCTCTGGA  
 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGCCCCAGAAC  
 CGAGTGCCATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCG  
 GGCCCTGCCATGTGCTGTAACGCATGCCTGGGTCTGCTGGGCTCTCCCACTCCAGCGGGA  
 CCTGGGGCGAGTGAAGGAAGCTCCCGGAAAGCAGAGGGAGCGGGTAGCGGCTGTG  
 TGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAGAACTGGAAGGAAGATGCTTTA  
 GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCATTATTCTG  
 GGAAGATGTTTTTCAAACCTCAGAGCAAGGACTTTGGTTTTTGAAGACAACAGATGATATG  
 AAGGCCTTTTGTAAGAAAAAATAAAGATGAAGTGTGAA

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MCSRVP LLLPL LLLL LALGPGVQGCPSGQCQSQ PQT VFTCTARQGT TVPRDVPD TVGLYVFEN  
GITMLDAGS FAGL PGLQL LDSLQNQ IASLPSGVFQ PLANLSN LDTANRLHEITNETFRGLR  
RLERLYLGKNRIRHIQPGAFD TDRLELKLQD NELRALPPLRLPR LLLDL SHNSLLALEP  
GILDTANVEALRIAGLGLQQLDEGLFSRLRN LHDLDVSDNQLERVPPVIRGLRGLTRLRLAG  
NTRIAQLRPEDLAGLALQELDVSNSLSLQALPGDLSGLFPRLRLAAARNPFNCVCLPSWFG  
PWVRESHVTLASPEETRCHFPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALS  
SSLAPTWSPTAPATEAPSPSTAPPTVGPVPQPQDCPSTCLNGGTCHLGRHHLACLCE  
GFTGLYCESQMGQTRPSPTPTPRPPRS LTLGIEFVPSVPLRGLQRYLQGS SVQLRSLRL  
TYRNLSDGPKDR LTLRLPASLAEYTA TLRLRNATVQLRVGRVPEGEACGEAHTPPA  
VHNSHAPVTQAREGNLPLLIALAAVLALAAVGAAYCVRGRGMAAAQDKGQVGPAG  
PLELEGVKVPLEPGPKATEGGEALPSGSECEVPLMGFPGLQSP LHA KPYI



**FIGURE 33**

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCAT  
 CTTTCATTCATTCATATGAGGAATAAGTGGTAAAAATCCTTGGAAAAACATGAGACTCATCAG  
 AAACATTTACATATTTTGTAGTATTGTTATGACAGCAGAGGGTGATGCTCCAGAGTGGCCAG  
 AAGAAGGGAACTGATGACCAACTGCTCCAACTGTCTCTAAGAAAGGTTCCCGCAGACTTG  
 ACCCGAGCCACACGACACTGGATTATCTATAACCTCTTTTCAACTCCAGAGTTTCAGA  
 TTTTCATTTCTGTCTCCAACTGAGAGTTTGTATCTATGCCATAACAGAAATCAACAGCTGG  
 ATCTCAAAAACCTTTGAATTCACAAAGGAGTTAAGATATTTAGATTGTCTAAATACAGACTG  
 AAGAGTGTAACTTTGGTATTTTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTTAATGACTT  
 TGACACCATGCTTCTGTGAGGAAGCTGGCAACATGTCACACCTGGAAATCCTAGGTTTGA  
 GTGGGGCAAAAATACAAAATCAGATTTCCAGAAAATTGCTCATCTGCATCTAAATACTGTC  
 TTCTTAGGATTCAGAAGCTCTTCTCATTATGAGAAGGTAGCTGCCCATCTTAAACACAAC  
 AAAACTGACATTTGTTTACCAATGGACAAAATTTCTGGGTTCTTTTGCCTGATGGAATCA  
 AGACTTCAAAAATATTAGAAATGACAAAATATAGATGGCAAAAGCCAAATTTGTAGTTATGAA  
 ATGCAACGAAATCTTAGTTTGAAGAAATGCTAAGACATCGGTTCTATTGCTTAATAAGTTGA  
 TTTACTCTGGGACGACCTTTTCTCTATCTTACAAATTTGTTGGCATACATCAGTGGAACT  
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTTGACTAC  
 TCAAAATCTGTAATGAGAACTATAAAATTTGGAGCATGTACATTTACAGAGTGTTTTACATTC  
 ACAGGATATAATCTATTGCTTTTGACCAAAATGGACATAGAAAACCTGACAAATCAAAATG  
 CCAAAATGCCACACATGCTTTTCCCAGAAATATCTCAGAAATTCCAATTTTAAATTTTGGC  
 AATAATATCTTAAACAGAGAGTTGTTTAAAGAACTATCCAACTGCTCCTGTTGAAAACCTCT  
 CATTTTGAATGGCAATAAATCGAGACACTTTTCTTAGTAAGTTGCTTTGCTAACACACAC  
 CCTTGGAAACACTTGGATCTGAGTCAAAATCTATTACAACATAAAATGATGAAAATTTGCTCA  
 TGCCGAAACCTGGGTCATATGAATCTGTCAACAATAAATGTTCTGATTTCTGTTCTCAG  
 GTGCTTGGCCAAAGATTTCAAATACTTGACCTAAATATAACCAAAATCCAAACTGTACCTTA  
 AAGAGACTATTTCACTGATGGCTTACGAGAATTAATATTGCAATTTTAAATTTTCTAAGTAT  
 CTCCTTGGATGTCAGTCAATTTGAGTAGACTTTCAGTTCTGAACATTGAAATGAATCTTATCT  
 CAGCCCATCTCTGGATTTTGTTCAGAGCTGCCAGGAAGTTAAACCTGCAATGCGGGGAAGAA  
 ATCCATTCGGGTGTACCTGTGAATTAATAAATTTTCATTTCAGCTTGAAACATATTCAGAGGTC  
 ATGATGGTTGGATGGTCAGATTCATACACCTGTGAATACCTTTAAACCTAAGGGGAACATG  
 GTTAAAGAGCTTTCATCTCCACGAATTTATCTTGAACACAGCTCTGTGATTGTCAACATTTG  
 TGGTTATTTATGCTAGTTCTGGGGTTGGCTGTGGCTTCTGCTCTCCACTTTGATCTGCC  
 TGGTATCTCAGGATGCTAGGTCAATGCACACAACATGGCACAGGTTAGGAAAACAAACCCA  
 AGAACCACTCAAGAGAAATGTCCGATTCACGCAATTTATTTATACAGTGAACATGATTTCT  
 GTGGGTGGAAGATGAATTTGATCCCCAATAGAGAAGGAAGATGGTCTCATCTTGATTTGCT  
 CTTTATGAAAGTACTTTTGACCTGGCAAAAGCATTAGTGAAAATATTTAAGCTTCAATTGA  
 GAAAAGCTATAAGTCCATCTTTGTTTGTCTCCAACTTTGTCCAGAAATGAGTGGTGCCATT  
 ATGAATTTCTACTTTGCCCCACCACAATCTCTTCCATGAAAATTTGGTTATTCCTTCTATA  
 TTACTGGAACCCATTCCTATTTGATTCATTTCCCAAGGATTCATAAATGAAAGCTCTCCAT  
 GGAAAAAAGCATATTTGGAATGGCCCAAGGATAGGCGTAATGTGGGCTTTTCTGGGGCA  
 ACCCTCTGAGCTGCTATTTAATGTTAATGTTATAGCCACAGAGAAATGTTATGAATCGAGACA  
 TTTACAGAGTTTAAATGAAGAGTCTCGAGGTTCTACAATCTCTCATGAGAACAGATTTGTCT  
 ATAAAATCCACAGTCTTTGGGAAGTTGGGGACCACTACACTGTTGGGATGTACATTTGATA  
 CAACCTTTCTACTTTGCCCCACCACAATCTCTTCCATGAAAATTTGGTTATTCCTTCTATA  
 TCGATTTCTAGAAGGATTTCTAAGAATGTATCCTATAGAAAACCTTTACAAGTTTATAAGG  
 GCTTATGGAAAAAGGTGTTTCATCCCAGGATGTTTATAATCATGAAAAATGTGGCCAGGTGCG  
 AGTGGCTCACCTTTGTAATCCCAGCACTATGGGAGGCCAAGGTGGGTGAGCCACAGAGGTCAA  
 GAGATGGAGACCATCTGGCCAAACATGGTGAACCCCTGTCTCTACTAAAAATACAAAATTA  
 GCTGGGGCTGTAGTGGTCAGCGCTGTAGTCCAGCTACTTTGGGAGGCTGAGGCGAGGAATCG  
 CTTGAACCCGGGAGGTGGCAGTTGTCAGTGAGCTGAGATCGAGCCATGCACTCAGCGTGTG  
 GACAGAGCGGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAAGAAAAAAGTGAACATCC  
 TCATGGCCCAAAAATAAGGTCTAATTCATAAATATATAGTACATTAATGTAAATATAATATA  
 CATGCCACTAAAAAGTAAGGTAGCTGTATTTTCTGGGTATGAAAAAACAATATTAATAT  
 GTTATAAACTATAGGTTGGTGCAAAACTAATTTGTTGGTTTGGCATGAAATGGCATTTGAA  
 ATAAAAGTGTAAAGAAATCTATACCAGATGTAGTAACAGTGGTTTGGGTCTGGGAGGTTGGA  
 TTAACGGGAGCATTTGATTTCTATGTTGTATTTCTATAATGTTTGAATGTGTTAGAATGA  
 ATCTGTATTTCTTTTATAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

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MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLT PATTTLDLSYNLLFQ  
LQSSDFHSVSKRLVLILCHNR IQQLDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL  
SFNDFDTMPICEEAGNMSHLEILGLSGAIKQSDFOKIAHLHLNTVFLGFRTLPHYEEGSLP  
ILNTTKLHIVLPMDTNFWVLLRDLGDKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL  
LNKVDLLWDDLFLILQFVWHTSVEHFQIRNVT FGGKAYLDHNSFDYSNTVMRTIKLEHVHFR  
VFYIQQDKYLYLLTKMDIENLTISNAQMPHMLFPNYPFKQYLYNFANNILTDELFKRTIQLP  
HLKTLILNGNKLETLSLVSCFANNTPLEHLDLSONLLQHKNDENCSPWETVVMNLSYNKLS  
DSVFRCLPKSIQIIDLNNNIQTVPKETIHLMALRELNIAFNFLTDLPGCSHFSRLSVLNI  
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLEYSEVMMVGWSDSYTCEYPLN  
LRGTRLRKDVHLHELSCNTALLIVTIIVIMLVGLAVAFCCFLHFDLPWYLRMLGQCTQTWHRV  
RKTTOEQELKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI  
VSFIEKSYKSIFVLPSPNFVQNEWCHYEFYFAHHNLFHENS DHIILILLEPIPFYCIPTRXHK  
LKALLEKKAYLEWPKDRKRCCGLFWANLRAAINVNVLATREMYELQFTTELNEESRGSTISLM  
RTDCL

GGGGGCTTTCTTGGGCTTGGCTGCTTGAACACTGCTCCAAGAACCGGCTCTGGAGGGGTCTCCGGAAAGG  
 GAGGAGAGAGGAGAGGCGGGGCGGGGCGGGGCGGGGCTGCGCGCTGCGCGCGCGCTCTGCGCGCCCTGTCCGCGCCGCG  
 CACGCCACGAGCGAGCCCGCGGGCGGCTCAGACGGCAGCGAGCGCGCGCTCTCCGCGCCAAAGCGCGCGCT  
 CTCTGCTGCGCTCGGCCCTTGCCCGCGCGAGCTTTCTGGCCGCGACCGCCCGCGCGCGCGCGCGCGTACCGTGA  
 CCTGCTCTGGGCGGGGCGAGCAGCAGCTGCTCCGCGCGGGGACGCTACCCACGCGTGGCCCTGTGCTC  
 CTGGAGTGAACCTTGGCGGGGTGGAGCGCCAGGGCGAGCCTCTGAGGACCGCTGATTATACGGGACGAGAT  
 CTGGAGCGGGAGGCTACTACGGCGCGGGAGCCGAGCTCGAGACTTCTCTCGCGCGCTGCTCGGGGCG  
 CGGGGAGGAGTGGGAGCGCGCGCGCGAGGAGCGAGCCAGGCGCCAAAGGGGCGACCAAGCGCAAGAAAGCTCCC  
 AAGAGGAGAGTGGCTCGGAGCGCTCCACAGGCTTAACACAGCAACAAAAAGTTATGAGAACAAAGT  
 CTCTGAGAAGCTGCCAAGCATGATACAGTGTCTGTGTGGCCGCGAAGATGTCCAGAGAGATTGCCCACTCT  
 TTGCTTGGAACCTTAAAAATCAGACTTCAGCTTCATGCTCAGCGTGAAGCGCTATGCGCTGGGGGCA  
 CATCGAGGAGATCAACATCCAGCGGGCATTAATAAAAATGTTTATGACGAGGCTGTGTGGCGGGGAG  
 AATGACTCCAGCATGGATTGAATGGTGTCTGGCGCTGACGAGTACTGGTGTATCATCATCAAGGA  
 CGAATCCCTCTGCTGAGTCACTGGGTGATATTAAGTGTATGTCAGCAATGACAGCCACAGCTGGGTG  
 ACTGTTAAGAATGCTGTGAGACTGATTTGAGGAAACAGTGAGAGAGATCTCTGTTCATAGAGCT  
 ACCGCTGCCCATGGTGGCCCGCTACATCCGATAAACCTCAGCTCGGTTGATATGGAGAGATCTGATCATGA  
 GATGGAGATCTGGGCTGCCACTGCCAGTCTAATTAATTTATCACCGCGGAACGAGATGACCACCT  
 GATGACTGGATTTTAAGCACCAATTTAAGGAATTCGCGCAGTTGATGAAAGTTTGAATGAATGTCTCC  
 CAATATCACCAAGATTTACAACTATGGAAAAGTCCACGGGCGCTGAAGCTGTATGCTGTGAGATCTCAGATC  
 ACCCTGGGAGCATGAGTCTGCGTGAAGCGGTTTCACTACATCTAGCGGGGCGACGGCAATGAGTCTGTGGC  
 CGGGAGCTGTGCTGTGCTGTGTCAGTGTCTGTGTTCAGGATACTTGGCGGGAATCGCGCATCTGCCACT  
 GGTGGAGGAGCGCGATTCAGCTCTCCCTCCTCAACCCGATGGGCTACGAGAAGCTCAGAAGGGGCTC  
 CGAGACTGGGAGCTGTGCTCGTGGAGCTGGGACCGATGGAATGACATCAACAACTACTTCTGATTTA  
 AACACGCTGCTCTGGGAGCAGAGATGACAGAAATGCCAGAGAAAGTTCCCATCACTATATGAGTACCTCC  
 TGAGTGGTTTCTCTCGAAAAATGCCAGCTGTGCTGCCGAGACAGCAGCTATACGCTGGATGGGAAAAATC  
 TTTTGTGCTGGGCGGAACTCGAGGCGGCGAGCTGTGTGTGGCTATPCTCAGAGCTGTGTGGCTCCCC  
 TGGAAAGCGGAGAACACCCCCACCCCGATGACCAGTGTCTCCGCTGGCTGCTATGCTCTCAC  
 ACACGCCCTCATGACAGCGCCGGAGGGGTGTGCCACAGGAGACTTCCAGAGAGAGGAGGAGCTGTCA  
 ATGGGGCTCTCTGGACACCGTCTCGTGAAGTGTGAACAGTTTCACTGATCTTCACTAAACTGCTTCGACTGT  
 TCATCTACGTGGGCTGTGATAAATACAGCATGAGGAGCTGCCCGAGGATGGGAGAAATACCGGAAATC  
 TCTGATCTGTCTCATGAGCAGGTTTCATGTTGGCATTAAGGCTTGTGAGAGATTCATGAAAAGAAATCC  
 CAACCGCTATTATCTCGTAGAGGACTGACATGACATPCAGACGCAAGTGGGGATATCGGCGCTCT  
 CTGAACTCCGTGGAGATATGTGCTCAGCAAGAAAGCGAAGTTTCACTGCCACAGAAGCTGATGTGTG  
 CTATGACATGGGGGCTCARGTGTGATCTTACACTTGAACAAACAGCATGGCCGAGATCCGAGAGATCATG  
 AGAAGTTTGGAGAGACCGCGTCAAGCTTCCGACGAGCGGCTGAAGCTCGGGGGCGGAAGAGACAGACGCT  
 GCGTGAACCTCTGGGCGCTTGAGACTCTGGGACATGCAAAATAAACAACTGGTATGCTCATATG  
 TGACTCACTCACTGTCTTTCTCTGTAATCAAGAAGTGCTCGAGAGAGGGTGATTTGGAGCGAGTCC  
 CAAAAGGAAAGCTGGAGCTGAGGCTGAGGCTTTCTTTCTTTCTGTCCATTACAAATTACTTGACAGAGCA  
 CGAGAGAAGCGATGGGAGTGAGAGAACTCAGCAAGCAACCTGGGAATCAGAGAGACGAGGAAGGAGG  
 GAGCTGTCTGCTTCAGAGCTCTGGCTCATGAGAAGAAATCTGGTGCTTTCTGTGCTGGACAGGCT  
 GTTCCAGTGGCTGTGCAATTTGCACAGCTAAATTCGAGATTTCCCGAGCTGGGCTGTCCAAATGTATACCA  
 TTTGAGATCGTCCGAGCGTCCAGAGAAATCCACCTCTCTGGCGGCGGACATTCGAAGCTGTACAAATA  
 ATTCTGTGTTCTTTGACATAGGCTCATTGGCAAGTGCATCAGTGAGCTCTTGATCTGTTTGAATCTCTCT  
 TTTTCAACAAAGGGGTGTTTCAAAAAGGAGAGAGGCTGAGATCATTCAGGAGTTGTTGGGACAGAGCA  
 TGAGCTCTTGCACAAAATTTGGTTCATAAAACCCCAAAGTCCCTGTGTATCCATAGGCTCGAGGTT  
 CCCCAGTAGGAGAGGACAGGATGCCAGCTCTCTGAGGCGCGAAATTTAGCTGGATCTCTCTTTTAC  
 CTGCTAGACTGGAAAGAGCCAGAATGGGGTGGCTCTGAGGCCCTCTCTGCTGAGTATGGCCCTGTGTG  
 GATTTGGCTCTCATGGTGGCCCATCATCAGCTGGGAGTTATTTTATATGTAGAATGCCAGATCTTCCA  
 GATTAGGCTTAATGTATTAACAACTCTTAGATATTCTGTGGACGATTCATTTGGGAGAAATATTGAATAT  
 CTCTGAGAAAAAGTTGTCTCATTTTGTTAATGTGTGCTCATTTGACTGGGAAAAATGAAAAAAAAA  
 AATAAGCAAAATGTAGACCTTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA

**FIGURE 36**

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPYARPEPELETFSPLP  
 AGPGEEWERRPQEP RPPK RATPKKAPKREKSAFEPPPPGKHSNKKVMRTKSSEKAANDDHS  
 VRVAREDVRESCPLGLETLKITDFQLHASTVKRYGLGAHRGLNIQAGINENDFYDGAWCA  
 GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSTWVTVKNGSGDMIF  
 EGNSEKEIPVLNELPVPMPVARYIRINPQSWFDNGSICMRMEILGCPLDPNNYYHRRNEMTT  
 TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF  
 HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNPDGYEKAYEGG  
 SELGGWSLGRWTHDGI DNNFPDLNTLLWEADRQNVPRKVPNHYIAIPEWFLSENATVAA  
 ETRAVIAWMEKIPFVLGGLNQGELVVAYPYDLVRS PWKTQEHTPTPDDHVFRWLAYSAST  
 HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFS YLHTNCFELSIYVGCDKYPHES  
 QLP EEWENNRESLIVFMEQVHRGIKGLVRDSHGKGIPNAIISVEGINHDIRTANDGDYWRLL  
 NPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTLSKTNMARI REIMEKFGKQPVSLPARR  
 LKLRGRKRRQRG

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**FIGURE 37**

CTAAGAGGACAAGATGAGGCCCGGCTCTCATTCTCCTAGCCCTTCTGTCTCTCCTTGGCCAAGCTGCAGGGG  
 ATTTGGGGGATGTGGGACTCCCAATTCCACGCCCGGCTTCAGCTCTTCCAGGTTGACTCCAGCTCCAGC  
 TTCAGCTCCAGCTCCAGGTCCGGCTCCAGCTCCAGCCGCGAGCTTAGGCAGCGGAGGTTCTGTGTGCCAGTTGTT  
 TTCCAAATTCACCGGCTCGTGGATGACCGTGGGACCTGCCAGTGTCTGTCTTCCCTGCCAGACACACCTTTTC  
 CCGTGGACAGATGGAAAGCTTGGAAATTCACAGCTCATGTTCTTCTCAGAGTTTGGAGAAAGAACTTTTAA  
 GTGAGGGAATATGTCCTAATTAATAGTGTGTATGAAAGAACTGTTAAACCTAACTGTCCGAATTGACATCAT  
 GGAGAGGATACCATTTCTTACACTGAATGGACTCGAGCTGATCAGGTAGAAGTGAAGGAGATGGAAAAAC  
 TGCTCATACAGCTGAAGGAGAGTTTGGTGGAGCTCAGAAATTTGTGACAGCTGGAGGTGGAGATGAAGAAAT  
 ATGACTCTCTTGGTAGAGAAGCTTGAGACACTAGACAAAAACAATTCCTTGGCATTGCCCGAGAATTCGTGGC  
 TCTGAAGACCAAGCTGAAAGAGTGTGAGGCCCTTAAGATCAAAACACCCCTGTCTGCTCCACCTCCCTCCACTC  
 CAGGAGCTGTGGTCTGTTGGTGGTGGTGAACATCAGCAAAACCGTCTGTGGTTGAGCTCAACTGGAGAGGGTTT  
 TCTTATCTATATGGTCTTGGGGTAGGGATTACTCTCCCGCATCCAAACAAGGACTGATTGGGTGGCGCC  
 ATTTGAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTACAACACACTGGATGATTGCTATTGTATATAA  
 ATGCTCGAGAGTTGCGGATCACCTATGGCCAGGTAGTGGTACAGCAGTTTACAACAACACATGTAGCTCAAC  
 ATGTACAACACCGGGAATATTGCCAGAGTTAACTTGACCACCAACAGATGCTGTGACTCAAACTCTCCCTAA  
 TGCTGCCATATAAACCCTTTTCATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGAATG  
 GATTGTGGTTATTATTCAACTGAAGCCAGCACTGGTAACATGGTGATTAGTAACTCAATGACACCACTT  
 CAGGTGCTAAACACTTGGTATACCAAGCAGTATAAACCATCTGCTTCTAACGCCCTCATGGTATGTGGGGTTCT  
 GTATGCCACCCGTACTATGAACACCAAGAACAGAGAGATTTTTTACTATTATGACACAAACAGGGAAGAGG  
 GCAAACTAGACATTTGTAATGCATAAGATGCAGGAAAAAGTGCAGAGCATTAACTATAACCTTTTGACCAGAAA  
 CTTTATGTCTATAACGATGGTTACCTCTGAATATGATCTTTCTGCTTTCGACAAGCCCCAGTAAAGCTGTTTA  
 GGAGTTAGGGTGAAGAGAAAAATGTTTGTGAAAAATAGTCTTCCCACTTACTTAGATATCTGCAGGGGTGT  
 CTAAGAGCTGTGTTCACTTTGACGCAATGTTTAGTGCATAGTTCTACCACTAGAGATCTAGACATTTGTCT  
 TGATTTGGTGAGTCTCTTGGGAATCATCTGCCTTTCAGGCGCAATTTTGCATAAAGTCTGCTAGGGTGGGA  
 TTGTCAGAGGTCTAGGGGCACTGTGGGCTAGTGAAGCCTACTGTGAGGAGGCTTCACTAGAAGCCTTAAATTA  
 GGAATTAAGGAACCTTAAACTCAGTATGGCGTCTAGGGATTCTTTGTACAGGAAATATTGCCCAATGACTAGTC  
 CTCATCCATGTAGCACCACTAATTTCTCCATGCTGGAAGAAACCTGGGACCTTAGTTAGGTAGATTAATATCT  
 GGAGCTCCTCGAGGGACCAATCTCCAACCTTTTTTTCCCTCACTAGCACCTGGAATGATGCTTTGTATGTGG  
 CAGATAAGTAAATTTGGCATGCTTATATATTCTACATCTGTAAAGTGTGAGTTTATGGAGAGAGGCTTTTT  
 ATGCATTAATTTGTACATGGCAATAAATCCAGAAGGATCTGTAGATGAGGCACTGCTTTTCTTTTCTCTC  
 ATTCTCCACCTTACTAAAGTCAGTAGAATCTTCTACCTATAACTTCTTCCAAAGGACGCTCAGATAGATTAG  
 AACCAGACTTACTAACCAATTCCACCCCCACCAACCCCTTCTACTGCCTACTTTAAAAAATTAATAGTTTT  
 CTATGGAAGTGAATCTAAGATTAGAAAAATTAATTTCTTAAATTCATTATGGACTTTTATTACATGACTCTA  
 AGACTATAAGAAAACTGATGGCAGTGACAAAGTGTAGCATTATTGTTATCTAATAAGACACTGGAGCATA  
 TTGCAACTTATGAGTGTATCAGTTCTGCTATGTAATTTTTTGCCTTTGTTTAAAGCTGGAACTGTGAAGAAAT  
 GAAAAATTTAAATTTTTTTCTAGGACGAGTATAGAAAGCTATTGAGAGTATCTAGTAACTCAGTGAGTAGT  
 TGGAAACCTTGGTGGTATGTATGTCTTCTGTCTTTGAATGACTTTATCATCTAGTCTTTGTCTATTTT  
 TCCTTTGATGTTCAAGTCTAGTCTATAGGATTGGCAGTTTAAATGCTTTTACTCCCTTTTAAAAATTAATGAT  
 TAAATGTGCTTTGAAAAAAGAAAAAAGAAAAAAGAAAAA

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**FIGURE 38**

MRPGLSFLALLFFLGQAAGDLGDVGPIPSPGFSSFPGVDSSSSSFSSSSSRSGSSSSSRSLGS  
GGSVSQLFSNFTGSDDRGTCQCSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYV  
QLISVYEKKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ  
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKECEASKDQNTFPVHPPPTPGSCGH  
GGVVNISKPSVVQLNWRGFSYLYGAWGRDYSPOHPNKGLYWVAPLNTDGRLLLEYRLYNTLD  
DLLLYINARELRITYGQSGTAVYNNNMVNMVNTGNIAVNLTTNTIAVTQTLPNAAAYNNR  
FSYANVAWQDIDFAVDENGLWVIYSTASTGNMVISKLNDDTLQVLNTWYTKQYKPSASNAF  
MVCVLYATRMTNTRTEEIFYYDYDNTGKEGKLDIVMHKMQEKVQSINYNPFDQKLYVYNDG  
YLLNYDLSVLQKPQ

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**FIGURE 39**

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCCTCTAAAGATCAAACACCCCTGTCGTCCAC  
CCTCCTCCCCTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT  
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC  
CCCAGCATCCAAACAAAGGNATGTATTGGGNGGCCCATTTGAATACAGATGGGAGACTGTTG  
GAGTATTATAGACTGTACAACCCACTGGATGATTGCTATTGTATATAAATGCTCGAGAGTT  
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA  
TGTACAACACCGGNATATTGCCAGAGTTAACCTGACC

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**FIGURE 40**

TCTCGCAGATAGTAAATAATCTCGGAAAGCGAGAAAGAAGCTGTCTCCATCTTGTCTGTAT  
 CCGCTGCTCTTGTGACGTTGTGGAGATGGGGAGCGTCTGGGGCTGTGCTCCATGGGCGAGCT  
 GGATACCACTGTTTGTGTGGAAGTGCCCGGTGTTTGCATGCCGATGCTGCTTGTAGGAAAC  
 AACTCCACTGTAACTAGATTGATCTATGCACTTTTCTTGCTTGTGGAGTATGTGTAGCTTG  
 TGTAAATGTTGATACCAGGAATGGAAGAACAACTGAATAAGATTCTGGATTTTGTGAGAATG  
 AGAAAGGTGTGTCCTTGTAAACATTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTT  
 GCTTTGGCTATGTTCTATCTCTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGA  
 TCCATAGAGCTGCAGTGCACAATGGATTTTGGTTCTTTAAATTTGCTGCAGCAATTGAACATTA  
 TTATTGGGGCATTCTTCATCCAGAAGGAACTTTACAACGTGTGTGGTTTTATGTAGGCATG  
 GCAGGTGCCCTTTTGTTCATCCTCATACAACCTAGTCTTACTTATTGATTTTGCACATTCATG  
 GAATGAATCGTGGGTGAAAAAATGGAAGAAGGGAACCTCGAGATGTTGGTATGCAGCCTTGT  
 TATCAGCTACAGCTCTGAATTAATCTGCTGTCTTTAGTTGCTATCGTCCTGTCTTTGTCTAC  
 TACACTCATCCAGCCAGTTGTTCCAGAAAACAGGCGTTCATCAGTGTCAACATGCTCCTCTG  
 CGTTGTGTGCTTCTGTAATGCTATATCTGCAAAAAATCCAAGAATCAACCAAGATCTGGTT  
 TGTTCAGCTCTTCAGTAATTACAGTCTACACAATGTATTTGACATGGTCAGCTATGACCAAT  
 GAACCAAGAAACAAATTGAACCCCAAGTCTACTAAGCATAAATTGGCTACAATCAACCAAGCAC  
 TGTCCCAAAGGAAGGCGAGTCAAGTGGTGGCATGCTCAAGGAATTTATAGGACTAATTC  
 TCTTTTGTGTGTGTATTTTATCCAGCATCCGTACTTCAACCAATAGTCAGGTATATAAA  
 CTGACTCTCAACAGTGATGAATCTACATTAAGAAGATGGTGGAGCTAGAAGTGTATGGAT  
 ACTGGAGGATGGGACAGATGTTCCAGGAGCTGTAGATAATGAAAGGGATGGTGTCACTTACA  
 AATCTCTTCCCTTCTTCACTTCTGCTTTTCTGGCTTCACTTTATATCATGATGACCCCTTACC  
 AACTGGTCCAGGATGAACCCCTCTCGTGAGATGAAAAGTCAGTGGACAGCTGTCTGGGTGAA  
 AATCTCTTCCAGTTGGATGGCATCGTGTGTATGTTTGGACACTCGTGGCCACCACTTGTTCT  
 TTACAAATCGTGATTTTGACTGAGTGTGAGACTTCTAGCATGAAAGTCCCACCTTTGATTATGC  
 TTTATTTGAAAACAGTATTTCCCAACTTTTGTAAAGTTGTGTATGTTTTGCTTCCCATGTAAC  
 TGTCCAGTGTCTGGCATGAATTAGATTTTACTGCTTGTGATTTTGTATTTTCTTACCAA  
 TGTCAATGTATGTGAAGTAGAATGAATTGCAGAGGAAAGTTTATGAATATGGTGTATGAGT  
 TAGTAAAAGTGGCCATTATTTGGGCTTATTCCTGCTCTATAGTTGTGAAATGAAGAGTAAAA  
 ACAAAATTTGTTGACTATTTTAAAAATATATTAGACCTTAAGCTGTTTTAGCAAGCATTTAAA  
 GCAAAATGTATGGCTGCCCTTTTGAATAATTTGATGTGTTGCCCTGGCAGGATACTGCAAGAAC  
 ATGGTTTATTTTAAAAATTTATAAACAGTCACTTAAATGCCAGTTTGTCTGAAAAATCTTATA  
 AGGTTTTACCTTGTATACGGAATTTACACAGGTAGGGAGTGTTAGTGGCAAAATAGTGTAGG  
 TTTATGGATGGAGGTGTCCGTACTAAATTTGAATAACGAGTAAATAATCTTACTTGGGTAGAGA  
 TGGCCTTTGGCAACAAAGTGAACCTGTTTGGTTGTTTTAAATCATGAAGTATGGGTTCAGT  
 GGAATATGTTTGAACCTCTGAAGGATTTAGACAAGGTTTTGAAAGGATAATCATGGGTAGAGA  
 AGGAAGTGTGTTTGAAGTCACTTTGAAGTTAGTTTGGGCCAGCAGCGTAGCTACCCCTT  
 GGTAATCCAGCACTTTGGGAGCTTAAGTGGGTAGATTACTTGAAGCCAGGAATTCAGACCA  
 GCTTGGGCACATGGTGAACCTGTTCTATAAAAAATATCTGGCTTTGAGCATATGCTCTGGTGC  
 CAGCACTGAGAGGCTAGTGAAGATTGCTGAGCCCAAGGCCAAGGTTGCAGTGAGCAAGTCA  
 CGTCACTGCACCTGTAGCTGGCAGAGATTAAGCCAAAAAATATATATATTTGAAATCAAGG  
 AGGCCAAATTTTGCAGGAAAGGAAGTAACTGCAAAACCACTAGGCTTTAGTAGGTACTTAT  
 ATAAAATCTAGTCCAGTTCTCTCATTAAAAAATGAAGACACTGAAATACAGACTTAAATA  
 GCTCAGATAGCTAAATTAGAAATTTCAAGTTGGCCAAATATAGCATCTCTCTGACATTTAA  
 AATATATTTCTATCAAAATACATGCATATTGATTTACACCTCATACTGTGATAAATTAATGT  
 ATGTGATTTGCTGGTGTCCAGCATGACCCATAAACAGGTGAGAAAGATGATGGAATGTTTT  
 AGAATAAATCTGCTTATAGTATACACAGTTCAAAGATGTTTTAAATGCTTTTGTAT  
 TTACTGCCATAGCTAAATGAAATATATAGATTATTTGAACCTTCAACCTGAAAAATCAAGCAGT  
 ATGAGGTTTGTGTTATTTGTTATGTGCTACTAGTGTCTAATGAGCTTTTAAATCTACAAAT  
 TCTCTTTTAAAAATTTTATTAATGTGAATGGAATATAACAATTCAGCTTAAATCCCCAAC  
 TTATCTGTGTGTAGACATTGTATCCACAATTTGATGGCTGTGTTTTACCTCTAAATAA  
 ATGAATTCAGAGAAAAA



**FIGURE 41**

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME  
EQLNKIPGFCENEKGVVPCNILVGKAVYRLCFGLAMFYLLSLLMIKVKSSSDPRAAVHNG  
FWFFKFAAAIAIIIGAFFIPEGFTTTFVWFYVGMAGAFCFILIQLVLLIDFAHSWNESWVEKM  
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLCVGASVMSI  
LPKIQESQPRSGLLQSSVITVYTMYLTSWAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV  
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLSDESTLIEDGGARSDGSLEDGDDVH  
RAVDNERDGVTSYSFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVWKISSSWIGI  
VLYVWTLVAPLVLNTRDFD

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**FIGURE 42**

GCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTGNGACGTTGTGGAGAT  
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC  
CCGTGTTTGCTATGCCGATGCTGTCCTAGTGGAACAANTCCACTGTAACTAGATTGATCTA  
TGCACTTTTCTTGCTTGTGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG  
AACAAGTGAATAAGATTCTCGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT  
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCT  
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGACAAATGGAT  
TTTGGTTCCTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

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GTATTATGTGAACCTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC  
CANGTTTGTGTGGAAGTGCCCCGTGTTTGNATGCCGATGCTGTCCTAGTGGAAACAANTCC  
ACTGTAATTAGATTGAATNATGCACPTTTNTTGCTTGTGTGGAGTANGTGTAGCTTGTGTAAT  
GTTGATACCAGGAATGAAGAACAACCTGAATAAGATTCTGGATTTTGTGAGAATGAGAAAG  
GTGTTGTCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG  
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG  
AGCTGCGAGTGCACAATGGATTTTGGTTTTTTAAATTTGCTGCAGCAATTGCAATTATTATTG  
GGGC

**FIGURE 44**

AAGAAGCTGTCTCCATCTTGCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC  
GTCCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTCCCCGTGTT  
TGCTATGCCGATGCTGTCTAGTGGAAACAACCTCCACTGTAAC TAGATTGATCTATGCACTT  
TTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC  
GAATAAGATTCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATTTTGGTTG  
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCTCTTTA  
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTT  
CTTTAAATTGCTGCAGCAATTGCAATTATTATTGGGGC

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**FIGURE 45**

GCTGTCCTTAGTGGAAACAANTCCAACCTTGTAACCTGGATTGATCTATGCACCTTTTCCCTTG  
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCAGGATTGGANGAACAACTGAATA  
AGATTCCCTGGATTTTTGTGAGAATGAGAAAGGTGTTGTCCCCTTGTAACATTTTTGGTTGGC  
TATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTCTTTACT  
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTTGGTTCT  
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACCTTTT  
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACAACCTAGT  
CTTACTTATTGATTTTGACATTATGGAATGAATCGTGGGTGAAAAAATGGAAGAAGGGA  
ACTCGAGATGTTGGTATGCAGCCTTGTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA  
GTTGCTATCGTCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTCAGAAAACAAGGC  
GTTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

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CTCGGGCGGCGCACAGGCAGCTCGGTTTGCCCTCGCATAGAGCTGCGGGTCCGGCCCGGGCGGGCTCTCCAAATCGGCAAAATGTGTGTGGCTGGAGCGCGAGCGCAGGCTTTCGGCAAGAGCGAGTCGAGTGTCTGTCAGACCGGGCGGACGTCCTGTTGAAGACGACATAAAGAAAAACATTATTAACTGTCATTACGAGGGGAGCGCCCGCGGGGTGCTCGCACTCCGCGCGGAACATTTGGCTCCCTCAGCTCCGAGACGAGGAGAAGAAAGCGGAAAGGAGCGAGATTCCATGTCGTTTCCAGCCAAAGTGGAATGATCGATGGCCCTCTGAAATTTATCAGATATTTGATTTATAGCATGCGCCCTGGTGTGTGTTACGCACACACATGTCGACCAAGGCTCTGGCTCGCTCTCTCCCTGTTTCCAGCTCTTGGGGTAATCCCAATCTGTTTCACTCTCCGCGAGGGCAGACGAGGAGCAGATGTCTGTGCAATCTCGGAGTGAAGAAGGCGAGGGAAGAAAGAACCAAGGACAGACCACTTGAGACTCCCAAAAGAACGACAGATCAGCAAAAAAGAGAGATGTCGGCCCGCGAGCTCTGTGCTGTGTTGCTGTCCCAACTGTGTTCTCTCTGTGGTGAAGCTCGGCCCTCTGTCTCGCACACCOCCTGTGAAGGACGTTTACAGGAGGACGCGAGAGCAATCCGCCCGCATCATCTCTGCTGTCTCAGGACACAGGATGTGGAGCTGGGTTTCATCAGGTGATGAACAAGACCGCGGCCATCATCGAGGACGGCGGGCGGCTCATCAACGCTCTGTGACCAACCAATGTGTCTGCCCTCAGCTCTCTCTCTCACTCTCGCAAGTAGCTCAACAACCAACACTCAACCAACCAATGAGAATGTCTCTGCCCTCTCTGGAGGCACAGCAGCAGAGCGCCACTTTCGCTGTCTTCAATGACCTGGTACCGACAGCTTTCTTCGGGAAGTAICTTTAATGATCAACGCGCTCTTAAGTGCACCGTGGTGAAGAGTGGTTCGAGATCTTAAAAACTCCGCTTTTATATATATACGCTGTGTTCGGAACGGGGTGAAGAGAAGCAGGACTCCGACTACTCAAAAGATTACCTCAACAGCTCATCAAAATGACAGGCTGAGCTTCTTCGCGAGCTCCAAGGATGATCCCGCACAGCCAGCTCTCTATGGTCACTCAGGCATCGAGCCCGCCAGCGCTCGAGGATCAGCCCATACGCTCTTCCCAAAGCGCTCATCAGCATACGCGGACTACAACTACGCGGCCCAAGCCCGGCACACCTTGATCTCGCATCGCGTCAATCGAGGACCCATGAAAGCCCATCCATGAAATCAACAACCTCTCAGCGGGAAGCTCTGCAGACCTCATGTCTGGTGTGACGATCATGGAGACGATTATAACATGCTGGTGAGACGGGGAGCTGGACACACCTGATCATCGACCGCGACCGTACACATCGGCACGTTGGCCTGTGAAAGGGAATCATGCGATTAGGTTTGACATCAGGGTCCCTCTTCTAGTGTGGCGGCCCAAGCTGGAAGCCGGCTGTGAATCCCAACTGTCTCAACATTGACCTGGCCCCAATCTGTGACATTCAGCGCTCGACATCTCCGGATATGACGGGAATCATCTCTCAAGCTGCTGGACACGCGCGGCCGTGAATCGTTTCACTTGAAGAAAGATGAGGGTCTGTGGCGGACTCTCTTGTGTGGAGAGGAGCGCTCTCAAGAGAGACATGACAGGTGACGCGCCAGGAGAGAACTTTTGCCCAATGTACGCGTCTGAAGGACTGTCTGAGCGTGTGCTAGGCTAGGACAGCGGCTGTGAGCACTGGGACAGACTGGGACAGACTGGGACAGTGTGGAGCGCCGCTGAGCTGATCAATGAGGAGTCAAGGCGCCACTCGGCTGTGGCGGCGGAGCGAGCCTCTTCCAACTCTGTGCGCAAGTCTGTGAGCGTGTGCTAGGCTAGGCTGTGACAGCGGGGACTCAAGACTAGCTTGGCGGCGGAGCGGAAAAAACTCTTCAAGGAAGAATCAAGGCGCAGCTATGTTCGCGATCGCTCTCATCGCTCATGCTGAGTGTGAGGTGCGGAGGTGTACCCAGTGTAGGCTGGGTGATCGCCGCCCGCCGAAACTCACTCAAGGCGGACTGTGGCGGGGCCCTGTGAGGCACAGATGACAAAGGTGTGGGGACTCATGGGACTGTGGGCTGTCCGGACTATCAGCGCCCAACCCCTTAAAGTGACATCTGGTGTGATCTCTTGAAGACGACACATGATGTGACCTGTGACATGTCTCAAGCTCTGAAAGCACAAGCTGTGACATCGACCAAGTGTAAACCTGCAGAACAAATTAAGAACCTGTAGGGAAGTCCGAGTCACTCACTGAAGAAAGCGGCCAGGAAGTGTGACGTGCACAAATGACTTACCACCCAGCACAAAGGCGCTCAAGCACAGGCTCCAGTCTGATCTGATCTTTGACGAAGGGCTCGAAGGAAGGACAGAGTGTGGCTGTTCGGCGACAGAGCCGAAGAAGAACTCCGCAAGCTGCTCAAGCGGCTCGCAGACACAGCAGCTGCAGCATGCCAGGCTCTTCTGTGCTGCACCGCGCCGACATTAACACGTACTGTGTCATGAGGACCATCAATGAGACTACAAATTCCTCTCTGTGAAATTTGCAACTGGCTTCTAGAGTACTTGAATCATACACAGACCCTTACCGTGAATGAATGACGTGAACACATGCAGAGGATGTCTCTCAACGAGCTACAGCTACAGCTCATGTAGGCTGTGAGGCTCGAAGGTTACAGAGCTGTAAACGCTCCGAGCTGAGCTGAGGTGAGCTATGAGCAATGAGCAATGAGCTGAGCTTTCAGCTCGAAAGTGGCCAGAAATGAAGAGACCTTCTTCCAAATCTGGGACAAGCTTGTGGGAAGCTGGGAAGGTGAAGAAATCAAGAGAGCTGGACCTCAAAAAGATAGAGGACTCACTGTCACAGCAATCAAAAAACAATGTGGGTGATTTTCAGAGAGCTGTGCTGATTTGGCAGGAGGCTCGAAGAGCAAGCAGCACTCATGTCACAGATTCGGAGATTCGAGATTTCTGGAGATTAACGACAGGACAGAGATGACATTCAGGAAGTCTATTTTGGCCCTGCTTTTGGCTTTGCTTTATATCTATATCTCACCAGTCCAGGCTGCACAAATGTCAATTTTTCGATTTCAAAAGTCAACCATACCCCTCCCGACAGCTCAAAAAGTCAAAAAGGAAAGCGGAGACAGGACAGAGATTTCTTGTGAAATTTCTTCCCAAGGGCGAAGTCAATGAAATTTTAAATCATAGGGGAAGACGCTCTCTCTTAAATCTTATTTCTTGGTTTGTGTCACAAAGGAAGTACAGAGACGAGCAGGACCACTGGAGAGGCTGAAACAGCTGCAGAGACGTTTGACAAATGAGTCACTGATCAAAAAGATGACATTTACTAGACATTAACCCCTGGTGCCTGTGAGAAACCTGCCCTCATTTGATATATGACTATTTACATGTAATCAATGGAACCTTTAGGCGAACCTTAATAAGAAATCCCAATTTTCAAGGCTGGTGTGTCATAAAGCTCTCTGGTGGCGAGTGTAAAAGAAA

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRNRNIRPNIIILVLTDDQDVELGSMQ  
VMNKTRRIMEQGGGAHFVTTMCCPSRSSILTKYVHNHNTYTNNENCSSPSWQAQHE  
RTFAVYLNSTGYRTAFEGKYLNEYNSYVPPGWEKVGLLKNSRFYNTLCRNGVKEKHGSD  
YSKDYLTLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRFLFPNASQHITP  
SYNYAPNPKHWMTRYTGPMKPIHMEFTNMLQRRKLQTLMSVDDSMETIYNMLVETGELINT  
YIVYTAHDGHHIGQFGLVGKGSMPYEFDIRVPFYVVRGNVEAGCLNPHIVLNI DLAPTILDI  
AGLDIPADM DGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNKDVAQEEN  
FLPKYQRVKDLCQRAEYQTACEQLGQKWQCVEDATGKLLHKCKGPMRLGGSRALSNLVPKY  
YGGGSEACTDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSV AIEVDGRVYHVGLGDAQ  
PRNLTKRHWPAPEDQDDKDGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDDL DLYKS  
LQAWKDKHLHI DHEIETLQNKIKNLREVRGHLKKRPEECDCHKISYTHQKRLKHGRGSSL  
HPFRKGLQEKKDVWLLREQRKKKLRKLRLQNNDTCSMPGLTCTHDNQHWKTAPFMTLG  
PFCACTANNNTYCMRTINETHLFLCEFATGFLFYFDLNTDPYQLMNAVNTLDRDVLNLQ  
HVOLMELRSCKGYKOCNPRTRNMDLDGGSYEQYROFORKRKWPCKRPSKSLGQLWEGWEG

**FIGURE 48**

AACAAAGTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA  
GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCCAGATGCTGGGCCTCCTGGGGAGCACAGCCC  
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTGCTGCTGCTGCTGCTGCTGGCCACC  
TGCCCTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA  
CCGAGTCCGCCGGGCCAGCCTTGGCCCTTCCGGCGGCGGGGCCACCTGGGAATCTTTCAAC  
ATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC  
CCCCGCCACACCCCTCACCACTCCACCACCACCACCACCCCCACCGCCACCATCCCCGCCA  
CGCTCGCTGAAGGCTGCTGTCGCCGGTGCTGTGGACAGCAGCTGCCCTGCCCTCCCATCTG  
TTCCCAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG  
GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGCATGCCCAGTGACTATATGGC  
AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGTGAAGGGTTTGGGGAGTGGAGAGCAAGG  
GTGCTCTTTCCGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCAGTGAGCCCCAGAAATG  
ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC  
ATCAGGCTGCTGCAGGCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCCTTTT  
GGTTTGGAGAAGGCAGTGTGAGGCTGCACAGTCAATTATCGGTGCCTTAGTCCAAGAAAAAT  
AAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 49**

MLGLLGSTALVGWITGA AVAVLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRAQPWPFR  
RRGHLGIFHHHRHPGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPHRHHPRHAR

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**FIGURE 50**

GCGGGCTGCTGAGCTGCCTTGAGGTGCAGTGTGGGGATCCAGAGCC**ATG**TCGGACCTGCTA  
 CTACTGGGCCTGATTGGGGCCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG  
 GTACTCAGGGCTACTGGCTGGGGTGAAGTGAGTGCTGGGTCACCCCCATCCGCAACGTCA  
 CTGTGGCCTACAAGTTCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCACTGAGAGC  
 TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC  
 CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC  
 CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC  
 CATGTGGTGACAGCCACCTTCCCCTACACCACCATTCTGTCCATCTGGCTGGCTACCCGCCG  
 TGTCCATCCTGCCTTGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGG  
 AGATCTACCAGGAAGACCAGATCCATTTTCATGTGCCCACTGGCACGGCAGGGAGACTTCTAT  
 GTGCCTGAGATGAAGGAGACAGAGTGGAATGGCGGGGCTTGTGGAGGCCATTGACACCCA  
 GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTCTCTGAAGCTTGGAAATGAGCC  
 CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTACCTGCGGCGAGCAGCCGTGGCTGGGAT  
 GACGGTGACACCCGACGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA  
 GGAGCTGGACTTGAGGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCCTGGGACTGAGC  
 CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCCTGAGAAGGGCAAGGAG**TAA**CCC  
 ATGGCCTGCACCCCTCTGCAGTGCAGTTGCTGAGGAAGTGCAGAGCTCTCCAGCAGACTCT  
 CCAGCCCTCTTCTCCTTCTCTGGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCCTGC  
 TCCAGGCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTAGGCTCCAGGGCCAGAGGAGCCA  
 GGGACTATTTTCTGCACACAGCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTC  
 ACAGTGGAGCTTCCAGGACCCAGAATAAAGCCAATGATTACTTGTTTACCTGGAACAAAAA  
 AAAAAAAAAA

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MSDLLLLGLIGLTLTLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGlyETGR  
LFTESCSISPKLRSIAVYYDNPHMVPPDKCRCAVGSILSEGEESPSPELIDLYQKFGKVFVS  
FPAPSHVVTATFPYTTLSIWLATRRVHPALDITYIKERKLCAYPRLIYQEDQIHfMCPLAR  
QGDFYVPEMKETEWKRWGLVEAIDTQVDGTGADTMSDTSVSVLEVSPGSRETSATLSPGAS  
SRGWDGDGTRSEHSYSESGASGSFELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEK  
GKE

**FIGURE 52**

CCGCGGGAACGCTGTCCTGGCTGCCGCCACCCGAACAGCCTGTCTGGTGCCCGGCTCCCT  
 GCCCCGCGCCAGTCA**ATG**ACCTGCGCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCT  
 GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA  
 CCTCCAAGTGGAGACCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGA  
 GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT  
 GACCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA  
 GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTAT  
 GGAAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT  
 GATTGCACTAATCCGAGCCAACCTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAG  
 GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAAT  
 AGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAAT**A**  
**A**TAAATAATAAATTTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

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**FIGURE 53**

MTLRPSLLPLHLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFCDTLHI  
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLDMCVGEKRRAIIPSHLAYGKRGF  
PPSVPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS  
KKKLKEEKRNSKKK

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**FIGURE 54**

CCCGGGAACGTGTTCTTGCGCTGCCGCACCCGAACAGCCTGTCTGCTGCCCGGCTCCCTGC  
CCCGCGCCAGTCATGACCCCTGCGCCCCTCACTCCTCCGCTCCATCTGCTGCTGCTGCTGC  
TGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC  
CTCCAAGTGAGACCCCTGGTGGAGCCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA  
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA  
CCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT  
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTATGG  
AAAACGGGGATTTCCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA  
TTGCACTAATCCGAGCCAACACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAGGG  
ATGGCCATGGTGCCACCCCTCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAATAGA  
CCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA  
AATAATAAATTTTAAAAAAGCTTA

**FIGURE 55**

CCGAAAGTCCCGTCCGGACCCCTCCAAGTGGAGACCCCTGGTGGAGCCCCAGAACCATGTGCC  
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG  
TATTATTGACACCTCCCTGACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA  
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT  
CCTTCTCACTTGGCCTATGGAACCGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGT  
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACACTACTGGCTAAAGCTGGTGAAGG  
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC  
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA  
CAAGAGCAAAAAGAAATAATAAATAATAAATTTAAAAAACTTAAAA

**FIGURE 56**

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTTTGTTCCTTGGCTAAAAATCGGGGGAG  
 TGAGGCGGGCCGGCGCGCGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG  
 ACCTGAAAAAAATGCTCTGGATTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG  
 GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGACTATTTTTTACAGGCTGGTGGAT  
 TATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCT  
 GTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA  
 GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTTTGGCTTTTCGTTGG  
 TTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTG  
 CTAAAGAAAAAGACATAGTATACCTGGAATTGCTGTATTTTCCAGAATGCCTTCATCTTT  
 TTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACGAAGACTTATGGCAGTGAACACATCTGAT  
 TTCCACAGCACAACAGCCCTGCATGGGTTGTTTGTTCCTTACTGCTCACTCCCAACCTT  
 TTGTAATGCCATTTTCTAACTTATTTCTGAGTGTAAGTCTCAGCTTAAAGTTGTGTAATACT  
 AAAATCACGAGAACACCTAAACAACAACCAAAAATCTATTGTGGTATGCACCTTGATTAACCT  
 ATAAAAATGTTAGAGGAACTTTACATGAATAATTTTGTCAAATTTTATCATGGTATAATT  
 TGTAAAAATAAAAAGAAATTACAAAAGAAATTATGGATTGTCAATGTAAGTATTTGTGCATA  
 TCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGTGTTTATTCAAATGTGGT  
 CTCTTCTGTGTCAAATGTTAAATGAAATATAACATTTTTTAGTTTTTAAAAATATCCGTGG  
 TCAAAATTCCTCTCACTATAATTGGTATTTACTTTTACCAAAAATTCGTGTAACATGTAAT  
 GTAACGGCTTTTGAGGGTCTCCCAAGGGGTGAGTGGACGTGTGGGAAGAGAGAAGCACCAT  
 GGTCCAGGCCACAGGCTCCCTGTGTCCCTTCCATGGGAAGGTCTTCCGCTGTGCCTCTCATT  
 CCAAGGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC  
 CACATCCACCACTG

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**FIGURE 57**

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWWIIIDA AVIYPTMKDFNHSYHACGVI  
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK  
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

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**FIGURE 58**

TTCTTGGCTAAAATCGGGGGAGTGAGGCGGGCCGGCGCGCGACACCGGGCTCCGGAACC  
ACTGCACGACGGGGCTGGACTGACCTGAAAAAATGTCTGGATTCTAGAGGGCTTGAGATG  
CTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC  
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT  
TTCACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGC  
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGCTCTGGGTCAACAGGTG  
CTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG  
ATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATT  
TTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGC

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**FIGURE 59**

TGGACGGACCTGAAAAAATGTTTGGATTNTAGAGGGNTTGAGATGTTTCAGAATGCATGAC  
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG  
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTTCAACCANTCATACC  
ATGCCTGTGGTGTTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA  
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTGGCTTTT  
CGTTGGTTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTGGAGGTT  
ATGTTGCTAAAGAAAAAGACATAGTATACCTGGAATTGNTGTATTTTTCCAGAATGCCTTC  
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

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**FIGURE 60**

GGACACCGGGTTCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAATGTTTGGATT  
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT  
CCATTGCTGCTGGTGACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT  
TATCCCACCATGAAAGATTTNAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGC  
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT  
GTTTGGGTCAAACAGGTGNTCGCATTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT  
CTGATTGNATTCTATGCGGATTCTTCTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT  
ACCCTGGAATTNCTNTATTTTTCCAGAATGCC

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**FIGURE 61**

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTCC  
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT  
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCTGTGGTGTATAGCAACCATAGCC  
TTCCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG  
TTTGGGTCAAACAGGTGNTNGCATTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN  
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC  
CCTGT

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**FIGURE 62**

GGGAGGCTGTGNCCTTTTGTNTTGGCTAAAATCGGGGAGTGAGGCGGCCCGGCGCGG  
CGNGACACCGGGTTCGGGAACCATTCACGACGGGTGGACTGACCTGAAAAAATGTTTG  
GATTTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATT  
GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT  
TATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCA  
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA  
GGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG  
ATNTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG  
TATACCTGGAATTGCTGTATTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

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**FIGURE 63**

CGACGCCGCGT**ATG**TGGCTTCCGCTGGTGCTGCTCCTGGCTGTGCTGCTGCTGCGCGTCC  
TCTGCAAACTTTACTTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTC  
AAACGGCCCCAGCGCCCTGTAACTGACAAGGAGCCAGGAAGAAGTTCTCAAACAAGC  
TTTTTTCAGCCAAACCAAGTGGCGGAGAAGCTGGATGTGGTGGAATTTGGCAGTGGCTTTGGGG  
GCTTGGCTGCAGTGCATTTAGCTAAAGCTGGCAAGCGAGTCTGGTGGCTGGAACAACAT  
ACCAAGGCGAGGGGGCTGCTGTACATCCTTTGGAAGAATGGCCCTTGAATTTGACACAGGAAT  
CCATTACATTTGGGCTATGGAAGAGGGCAGCATTTGGCCGTTTTATCTTGGACAGATCACTG  
AAGGGCAGCTGGACTGGGCTCCCCCTGCTCTCTCTTTTGACATCATGGTACTGGAAGGGCCC  
AATGGCCGAAGAGTACCCCATGTACAGTGGAGAGAAAGCTACATTCAGGGCCTCAAGGA  
GAAGTTTCCACAGGAGGAAGCTATCATTGACAAGTATATAAAGCTGGTTAAGTGGTATCCA  
GTTGAGCCCCCTCATGCCATCCTGTTGAAATTCCTCCATTGCCGTGGTTCAGCTCCTCGAC  
AGGTGGGGCTGCTGACTCGTTTCTCTCCATTCTTCAAGCATCCACCAGAGCCTGGCTGA  
AGTCTCGACAGCTGGGGGCTCCTCTGAGCTCCAGGCAGTACTCAGCTACATCTTCCCCA  
CTTACGGTGTCAACCCCCAACACAGTGCCTTTTCCATGCAAGCCCTGCTGGTCAACCACTAC  
ATGAAGAAGGCTTTTTATCCCCGAGGGGTTCCAGTGAATTTGCCCTTCCACACCATCCCTGT  
GATTCAGCGGGCTGGGGGCGCTGTCTCACAAGGCCACTGTGCAGATGTGTTGCTGGACT  
CAGCTGGGAAGCCTGTGGTGTCAAGTGTGAAGAGGGGCATGAGCTGGTGAACATCTATTGC  
CCATCGTGCTCTCCAAAGCAGGACTGTTCAACACCTATGAACACCTACTGCCGGGGAAGCG  
CCGCTGCTGCCAGGTGTGAAGCAGCAACTGGGGACGGTGGGCCCGGCTTAGGCATGACCT  
CTGTTTTATCTGCTGCGAGGCACCAAGGAAGACCTGTCATCTGCCGTCCACCACTACTAT  
GTTTACTATGACACGGACATGGACCAGGCGATGGAGCGCTACGCTCCATGCCAGGGAAGA  
GGCTCGGGAACACATCCCTCTCTCTTCTCGCTTTCCCATCAGCCAAAGATCCGAGCTGGG  
AGGAGGATTTCCAGGCCGCTCCACCATGATCATGCTCATACCCACTGCCTACGAGTGGTTT  
GGAGAGTGGCAGCGGAGCTGAAGGGAAAGCGGGGCAGTGACTATGAGACCTTTCAAAAACCT  
CMTTGTGGAAGCCTCTATGTCACTGGTCTGAAACTGTTCCCACTGGAGGGGAAGGTGG  
ACAGTGTGACTGCAAGGATCCCCACTCACCACCAAGTTCTATCTGGCTGCTCCCCGAGGTGCC  
TGCTACGGGCTGACCATGACCTGGGCCGCTGCACCTTGTGTGATGGCCTCCTTGAGGCG  
CCAGAGCCCCATCCCCAACCCTATCTGACAGGCAGGATATCTTCACTGTGGACTGGTGG  
GGGCCCTGCAAGGTGGCCTGCTGTGCAGCAGGCCATCCTGAAGCGGAACTTGACTCAGAC  
CTTAAGAATCTTGATTCTAGGATCCGGGCACAGAAAGAAAAGAAAT**TAGT**TCCATCAGGGAGG  
AGTCAGAGGAATTTGCCCAATGGCTGGGCACTCTCCCTTGACTTACCCATAATGTCTTTCTG  
CATTAGTTCCTTGACAGCTATAAAGCACTCTAATTTGGTTCTGATGCCTGAAGAGAGGCCCTAG  
TTTTAAATCAAAATCCGAATCTGGGGCAATGGAATCACTGCTTCCAGCTGGGGCAGGTGAGA  
TCTTTACGCCTTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATAGCTTGATG  
TCTCATGACGAGCGGCGCTCTGCATCCCTCACCATGCTCTCCTAATCACTGATGATCAAGCGA  
ATATTCCATCTGTGGATAGAACCCCTGGCAGTGTGTGCTCAGCTCAACCTGGTGGGTTGAGTTG  
TGCTCTGAGCTTCTGCTCTCATTTAGTGCTACGCTGCACAGTTCTACAGTCAACAGG  
GAAAAGGGAGCTAATAGGGCTTAACTCAAAACCTGGGCGTGGTTTGGTTGCCATTCATA  
GGTTTGGAGACTCTAGATCTCTTTTGTGCTGGGTTTCACTGGCTCTTCAAGGGGACAGGAAT  
GCCGTGTCTGTGGCAGTGTGGTTCTGGAGCTTTGGGGTAACAGCAGGATCCATCAGTTAGTA  
GGGTGCATGCAGATGATCATATCCAATTATATGGAAGTCCCGGCTCTGTCTTCTTTATCA  
TCGGGTTGGCAGCTGGTTCTCAATGTGCCAGCAGGGACTCAGTACTGAGCCCTCAATCAAGC  
CTTATCCACCAAAATCAGCGGAAGGTTGATGCAAGGAAGGGTGACATCAGGAGTCAGGGCA  
TGGACTGGTAAGATGAATCTTGTCTGGGCTGAAGCAGGCTGCAGGGCATTCCAGCCAAGGG  
CAGACGAGGAGGAGCTGCAGGAGGTTGGGGTAAGGGGAAGGTAACATCAGATAAGAAAGGA  
AAGCCACGGAAATGTGTGTGAAGCCAGAAATGGCAATTTGCAGTTAATAGCACATGTGAGGG  
TTAGACAGGTAGTGAATGCAGCTCAAGGTTTGGAAAAATGACTTTTCACTGTTATGCTTGT  
GTATCAGACATACGAAAGGCTCTCTTTGATGTTCTGTTAATGTAACATTAATAAATTTATTG  
ATTCCATTGCTTTAAAAA

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**FIGURE 64**

MWLPLVLLLAVLLLAVLCKVYLGLFSGSSPNPFSEVDKRPAPLVTDKEARKKVLKQAFSAN  
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG  
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNRKEYPMYSGEKAYIQGLKEKFPQ  
EEAIIIDKYIKLVKVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ  
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHMKGGFYPRGGSSEIAFHTIPVIQRA  
GGAVLTkATVQSVLLDSAGKACGVSVKKGHELVNIYCPIVVSNAGLFNTYEHLLPGNARCLP  
GVKQQLGTVRPGLGMTSVFICLRGTKEDLHLPSTNYVYYYDTMDQAMERYVSMPPREAAEH  
IPLFFAFPSAKDPTWEDRFGRSTMIMLIPTAYEWFEWQAEKKGKRGSDYETFKNSFVEA  
SMSVVLKLFQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI  
PNLYLTGQDIFTGCLVGALQGALLCSSAILKRNLYSDLKNLDSRIRAQKKKN

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**FIGURE 65**

GCAGCGGCGAGGCGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCTA  
 GGGGTTGGCACCGGCCCCGAGAGGAGG**ATG**CGGGTCCGGATAGGGCTGACGCTGCTGCTGTG  
 TCGGGTGGCTGCTGAGCTTGGCCTCGGCGTCTCGGATGAAGAAGCAGCCAGGATGAATCCT  
 TAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTAAAGGACCATACTACTGCAGGCAGA  
 GTAGTTGCTGGTCAAATATTTCTTGATTGAGAAGAATCTGAATTAGAATCCTCTATTCAAGA  
 AGAGGAAGACAGCCTCAAGAGCCAAGAGGGGAAAGTGTACAGAAGATATCAGCTTCTCTAG  
 AGTCTCCAAATCCAGAAAAACAAGGACTATGAAGAGCCAAAGAAAGTACGGAACACAGCTTTG  
 ACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCTTTCTTAGATAA  
 GGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTGCTACAACCT  
 ATGACTACAAAGCAGATGAAAAGTGGGGCTTTTGTGAACTGAAGAAGAGGCTGTCTAAGAGA  
 CGGCAGATGCAGGAAGCAGAAATGATGTATCAAAGTGAAGTGAAGTCCCTAATGGAAGCAA  
 TAAGAAAAGCCAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAGCATGAACCATA  
 CCAAAGCCCTGGAGAGAGTGTATATGCTCTTTTATTGGTGATTACTTGCCACAGAATATC  
 CAGGCAGCGAGAGAGATGTTTGAAGAGCTGACTGAGGAAGGCTCTCCCAAGGGACAGACTGC  
 TCTTGGCTTCTGTATGCCTCTGGACTTGGTGTTAATTCAAGTCAGGCAAAGGCTCTTGAT  
 ATTATACATTTGGAGCTCTTGGGGCAATCTAATAGCCACATGGTTTGGTAAGTAGACTT  
**TAGT**GGAAGGCTAATAATATTAAACATCAGAAGAATTTGTGGTTTATAGCGGCCACAACCTTT  
 TCAGCTTTCATGATCCAGATTTGCTTGATTAAGACCAAATATTCAGTTGAACCTCCCTCAA  
 ATTCTTGTTAATGGATATAACACATGGAATCTACATGTAATGAAAGTTGGTGGAGTCCACA  
 ATTTTCTTTAAATGATTAGTTTGGCTGATTGCCCCATAAAAGAGAGATCTGATAAATGGC  
 TCTTTTTAAATTTTCTCTGAGTTGGAATGTGAGAATCATTTTTTACATTAGATTATCATAA  
 TTTTAAAAATTTTCTTTAGTTTTTCAAATTTTGTAAATGGTGGCTATAGAAAAACAACAT  
 GAAATATTATACAATATTTGCAACAATGCCCTAAGAATGTGTAATTCATGGAGTTATTT  
 GTGCAGAAAGTCTCCAGAGAGCTCTACTTCTGTTTTTACTTTTTCATGATTGGCTGTCTTC  
 CCATTTATTCTGGTCATTTATTGCTAGTGACACTGTGCCTGCCTCCAGTAGTCTCATTTTCC  
 CTATTTTGCTAATTTGTTACTTTTTCTTTGCTAATTTGGAAGATTAACTCATTTTTTAATAAA  
 ATTATGTCTAAGATTAAAAA  
 AA

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**FIGURE 67**

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT  
GCCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCT  
GTCAGTTTCCCAGACAGTCTTGCCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG  
CTCAACTCTCCTGCACGCTCAGCCCCCAGCACGTCACCATCAGGGACTACGGTGTGCCTGG  
TACCAGCAGCGGGCAGGCAGTGCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA  
CCACCGGCCTGTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCCAATGCCT  
GTGTCTCTACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC  
TACGGCTTTAGTCCCTAGGGGTGGGTGTGAGATGGGTGCCTCCCTCTGCCTCCCATTTCT  
GCCCCTGACCTTGGGTCCCTTTTAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAATGGG  
TTAATAATATTCAACATGTCAACAAC

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**FIGURE 68**

MACRCLSFLLMGTFLSVVSQTVLAQLDALLVFPQQVQLSCTLS PQHVTIRDYGVSWYQQRAG  
SAPRYLLYYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVQPEDDADYYCSVGYGFS P

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**FIGURE 69**

GCGCGCCCCGCCCGAGACCGGGGCCCGGGGCGCGGGGCGCGGGATGCGGCGCCCCGGGGCGG  
 CGATGACCGCGGAGCGCAGCGCGCGGCGCGCCCTGACCCCGCGCCGCGCGCTGAGCCCC  
 CCCGCGAGGTGTCGGGACAGGCCGAGATGACGCGCGAGCCCTGTGTGCTGCTCTGCTGCGCG  
 CGCTGCTGCTGGGGGCGCTTCCACCGCGCGCGCGCGCGCGGAGGCGCCCCAAGATGGCGGAC  
 AAGGTGGTCCACCGCAGGTGGCCCGGCTGGGCGCACTGTGCGGCTGCAATGCCAGTGGGAGGGA  
 GGGGGACCGCGCGCTGACCATGTGGACCAAGGATGGCGCACCATTCCACAGCGCGCTGGA  
 GCGCGCTTCCGCTGCTGCGCGAGGGGCTGAAGGTGAAGCAGGTGGAGCGGGAGGATGCCGGC  
 GTGTAGTGTGCAAGGCCACCACCGCTTCGGCAGCCTGAGCGTCAACTACACCTCTGTCGT  
 GCTGGATGACATTAGCCACGGGAAGGAGAGCCTGGGGCCGACAGCTCTCTGGGGGTCAAG  
 AGGACCCCGCAGCGCAGCTGGGCACGACCGCGCTTACACAGCCCTCCAAGATGAGGCGC  
 TCGGTGATCGCAGCGCCGTGGGTAGCTCCGTGCGGCTCAAGTGGTGGCCAGCGGGCACCC  
 TCGGCTCGACATCAGCTGGATGAAGGACGACAGGCTTGAACGCGCCAGAGGCGCGTGAAG  
 CCAGGAGAAGAAGTGGACACTGAGCCTGAAGAACCTGCGCGCGGAGGACAGCGGCAAAATAC  
 ACCTGCGCGGTGTGAACCGCGCGGGCGCCATCAACGCCACCTCAAGGTGGATGTGATCCA  
 GCGGACCGCTTCCAAGCCGTGCTACAGGCACGACCCCGTGAACACGACCGGTGGACTTCG  
 GGGGACACCGCTCTTCCAGTGAAGGTGCGCAGCGAGCTGAAGCCGGTGTGATCAGTGGCTG  
 AAGCGCTGGAGTACGGCGCGGAGGGCGCCCAACTCCACCATCGATGTGGGGCGCCAGAA  
 GTTTTGTGGTCTGCCACCGGGTGACGTGTGTGCTGCGCGCGCGCGCTCTTCACTCAATAAGC  
 TGCTATCACCGCTCCCGCGCAGGACGATGCGGCGATGTACATCTGCTTTGGCGGCCAACCC  
 ATGGGCTACAGCTTCCGCGCGCTTCTTCCACCGTGTGCGCAGCGCAAAAACCGCGAGGGCC  
 ACCTGTGCGCTTCTGCTCTGCGCCTAGCTTCCGCTGCGCGCTGCTCATCGGCATCCGAC  
 CGCGCGCTGTCTTCACTTCTGGGCACCTGTCTGTGGCTTTGCCAGGCGCCAGAGAAGCGCG  
 TGACACCGCGCGCGCTGCGCTTCTGCTGGGCGACCGCGCGCGGAGCGCGCGGACCGG  
 GCGCGAGACAGGAGCTTCTTCTGCTGGCGCGCTTACGCGTGGCGCTGGTGTGGGGCTGT  
 GTAGGAGCATGGGTCTCGCGACGCGCGCGCGCTTACTGGCGCGCGCGCGCTGGTGTGGT  
 CCTAAGTGTGACCGCAACTCTACACAGACATCCACACACACACACACACACTCTCACAC  
 ACATCTACAGCTGGAGGCGAAGGTCCACGACATCCACTATCACTGTCTAGACGGGCGCGCT  
 ATCTGACTGGGCACGGGGGGCGCGCGCAGACAGGACAGTGGGAGGATGAGGAGCGAGGCT  
 GCAGACGAAGGCGAGGGGACCCATGGCGAGGAGGAATGGCCAGACCCGAGCGAGTCTGTGTG  
 TGAGGCATAGCCCCCTGGACACACACACACAGACACACACACTACCTGGATGCATGTATGAC  
 ACACATCGCGCGACACGCTCTCTTGAAGGCACACGTCACGACACGCATGTGCACAGATATG  
 CCGCTTGGGCACACAGATAGCTGCTGCTGGACGCACACAGTGCAGATATGGTATCCGGACACA  
 TACAAGGACATGCTGCTGAACATACACAGCAGACCCATGCGCAGATGTGCTGCTGGACA  
 CACACACACACAGGATATGCTGTCTGGACGCACACAGTGCAGATATGGTATCCGGACACA  
 CAGTGCACAGATATGCTGCTGGACACACAGATAATGCTGCTTGCACACATGACAGGATGCA  
 ATATTGCTTGGACACACACACACACACGCGTGCACAGATATGCTGCTTGGACACGACAC  
 ACATGCAGATATGCTGCTTGGACACACACTTCCAGACACAGTGCACAGGCGCAGATATGCT  
 GCCTTGGACACAGCAGATATGCTGTCTAGTACACACACACGACAGATGCTGTCCGGACAC  
 ACACACGCGATGCAGATATGCTGTCCGGACACACACACGCGAGATATGCTGCGGATACACAG  
 ACACACACAGATAATGCTGCTCAACTACACACGTCGAGATATGCTTGGACACACACAC  
 TGTGCACAGATATGCTGTGTCAGATGACACACAGTGCAGATATGCTGTCCGGACACACG  
 CAGGACACACATGAGATATGCTGCTGGGACACACTTCCGGACACACATGACACACAGGAT  
 GCAGATATGCTGCTGGACACACACACAGATAATGCTGCTCAACACTACACACGTCGAGTA  
 TATTGCTTGGACACACATGTCAGATATGCTGTGTCGACACACACAGTGCAGATA  
 TGCTGTCCGGATACACGACGACACATGACAGATATGCTGCTGGGACACACTTCCGGAC  
 CACACATGCACACAGGTCAGATATGCTGCTGGACACACGACGACGATGACGTGCTTTGG  
 GAGGCTGTCCGCTGAAGCTGCTGAGTACGTGTGCGGTGAGGCTCATAGTTGATAGGGAGCTT  
 CCCTGCTCCACCGTCACTCCCCAACTCTGCGCGCTCTGTCCCGCTCACTAGTCCCCGCTC  
 CATCCCGCTCTGTCCCTGGCTTGGCGGCTATTTTGGCACTGCTTGGTGGGCGCCAGG  
 AGTCCCCCTACTGCTGTGGGTGGGGTGGGGGACAGCAGCCCAAGCCTGAGAGGCTGGAG  
 CCGATGGCTAGTGGCTCATCCCGAGTGCATTCTCCCGTGCACAGAGAAGGGGCGCTGGTA  
 TTTATATTAAAGAAATGAAGATAATATTAATATGATGGAAGGAAGACTGGGTTGCAGGGAC  
 TGTGGTCTCTCTGGGGCGCGGACCCGCGCTGGTCTTTCAGCCATGCTGATGACACACCC  
 GTCCAGGCGCAGACACACCCCGCAGCTGTGCTGGTGGCGCCAGATCTGTGTAATTTTA  
 TGTAGAGTTTGAAGTGAAGCCCGTATATTTAATTTATTTTGTAAACACAAA

MTTPSPLLLLLLPLLLGAFPPAAAAAGRPKMKADKVVPRQVARLGRTVRLQCPVEGDPPPLTM  
WTKDGRTHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVLDDISPGK  
ESLGPDSSSGGQEDPASQQWARPRFTQPSKMRVRVIARPVGSSVRLKCVASGHPRPDITWMK  
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTSRKPV  
TGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFFVLP  
TGDVWSRDPGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPKPPGPPVASSSSA  
TSLPWPVVIGIPAGAVFILGTLTLWLCAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPS  
LAALSAGPGVGLCEEHGSAPAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHTHSHVEGKV  
HQHIHYQC

**FIGURE 71**

CCGAGCTGAGGAGCCCTGCCTAAGACACGGTCACTGGATCTGAGAACTTCCGAGGGGACCGCATTCCAGAGTCT  
 AGTGAATCTGTGGAAGCCACCATCTACCTCTTGCCACGTTCCACGGGCTTGGGGGAAAGATGCTGGGGGACCA  
 GAGCTGGGTGTTTCTCTTCTGGTCTGGGAAGTACATCTGTGTTGGGGAGACAGACGATGCTCACCGATCA  
 GTAAGAAGATCCAGGCTGGGAAGAAGAACCCGACATCTTTGCAAGGCTGCCGACACCTGGAGAGCCCTG  
 TGAGTGGACAACTGGTTCAACATCGACTACCCAGGCGGGAGGGGACATCTACAGGCGTGGAGGCTGATGCT  
 TCTACTATGGGACGCTGATGATGTCCTCCCTGCGGCTGACAGCTCGACACTGACTTGGACACTCTGGGGG  
 AGCTACTGCCAGCTGGTCACTGATGTTCCCGTGGAGGTTTCTGGTGCTTCAACAGGAGGACGCGGCTGGCCA  
 GAACCTGCTTAATTACACCGTAGCTCTCTCTGCCACCAGGATCCCTGCCGAGACACAGAGCGCATCTGGA  
 GCCATGGTCTCCTTGAGGAAAGTGTCTGAGTGCCTGCTGGTGGTCACTGGGGTCCAGACTCGCACACGCAATTTGC  
 TTGGCAGAGATGGTGTGCTGCTGTCGATGAGCCAGCGAAGAGGGTCACTGCTGGGCGAGGACTTACAGC  
 CTGTGACCTGACTGCCCAATGGGCGAGGTGAATGCTGACTGTATGCTGATGCTGATGCTGATGCTGATGCTG  
 ATGGGGCTGTATCGTCCGAGGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
 CTG  
 GATCAAAAGGTCAAGTTGCCCTTGTACTCAAAATGCCAAGACTAGCTGAAGGCGAGCCACATCAAGG  
 CAGAGTTTGTGAGGCGAGAGACTCCATACATGTTGATGAACCTGAGACAAAAGACCGAGAGCTGGGCGAGG  
 GTGCTCTGTGCTGCTGAAGGCCACAGGGAAGCCAGGCCAGACAGTATTTTGGTATCATTAATGACACATTTGCT  
 GGAATCCCTTCCCTTACAGACTGAGAGCAAGCTGGTCTGAGGAAATCGCAGAGCAGCAGGCTGGGAGTACT  
 TTTGCAAGGCGCAGAGTGATGCTGGGCTGTGAATTCGAGGTTGCCGAGCTGATTTTCACAGCATCTGATGAG  
 ACTCTCTGCAACGAGGCTCTGAGAGCTATCTTATCCGGCTGCCCATGATTGCTTTCAGAAATCCAGCAACT  
 CTCTACTATGACGTGGGAGCGCTGCCCTGTTAAGACTTGTGCGAGGCGAGGAGATATGGGATCAGGTGGCGTG  
 ATGCTGTGCAAGACTGCTGTGGGACTTCCAAGACAGGGAAGGAGATCCAGTGGTGGCTACAGCTTACCCT  
 ACCAAGGTGGCCAAAGGTGACGCTGCCAGCGGTGTACGGAACTCGGAGCATCGTGGGGGCGCTGTGACTGCT  
 TGCTGACAAATGGGAGCCCATGCGCTTTGGCCATGTGTACATGGGAGCAGCGCTGTAAACCATGACTGGCTACA  
 AGGCACTTTACCTCTCATGCTCCGAGAGCTAGAGGCTGGTCTCAATTTGTGACAGCTGCGAGAG  
 TTTGTCAACACCAAGGTGCTACTTTCAACAAGAAGGGAGTGCCGTGTTCCATGAATCAAGTGTCTTGT  
 TCGGAAGAGCCCATGAGTTTGAAGCCATGGAGACCAACATCATCCCTGGGGGAGATGGTTGGTGAAGAC  
 CCATGGTGAATCGACTTCCATCCAGGAGTTTTCACAGCAAGATGGGAGGCCCTACATAGAGAAAGTGAAG  
 GCGGACTGTACCTTCTGGATCCCGGAATATTTCAACAGCCAGAGCTGCCAGACTGCCCAGACTTCAATCA  
 TGACGAGAGGAGACACTTTCCCTTTCGAGCATATGCTGTTCTGTGGAATTCAGAGATGAGTCACTCA  
 AGCCACTTAATGCTGGCAAGGTGAGGCTCAACCTGACTCAACCCAGGTCAAGTGGCCAGAGACATATCCACA  
 CTGAAACTCTGCTCACTCAATCCAGACACAGGGCTGTGGGAGGAGAGGATGATTCAAATTTGAAATCAAG  
 GAGGAACAAAAGAGAGAGCAACCTTCTGGTGGGCAACCTGGAGATTGCTGAGAGAGGCTCTTTAACTGG  
 ATGTTCTGTAAGAGCAGCGCGTCTTTGTTAAGGTGAGGCGCTACCGGAGTGAGAGGTTCTTGCTAGTGAGCAG  
 ATCCAGGGGGTGTGATCTCCGATTAACCTGGAGCCTAGAGACTTGTCTGTGCTCAACCTAGGAGGCTGGG  
 CGGCTTTGACAGTGTGATCAGAGGCCCAAGGGGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT  
 CTTACTCTGCTATCTTTGCTAGCTCTGGCTGGGAGGAATCGAAGCAGTGGAGTCTTCTCTAAATTCAC  
 CCAAAATGCAATTTGGGCTCCCTCAGGCCCTATCTCAACAAGCTCAACTACGCTCGGAGCGGACATGGGATCCAG  
 GGTAAAAAGACAGCTTTCCAGATTAGCATGGCCAAAGCCAAAGCCCACTCAGCTGAGGAGAGCAATGGGCCA  
 TCTATGCTTTGAGAACTCTCGGCGATGTGAAGAGGCACCCAGTGCAGGCCCTCTCGGTTTACGAGATT  
 GAGGGGGATCGATATGACTACACAGCTGCCCTTCAAGCAAGTGAACCTATGAGCTGAGCTGAGCTGAGCTGAT  
 GCGATGTGGCCAAAGCGATGATGAGGCTCTTATCAAGTGAAGATTGTGGGGCCATCGGAAGTGT  
 ATGTGCGATCCCGCAACATGGGGGCACTCATCGGCGGACAGTGGGGAAGCTGTATGGAATCCGAGATTGTGAGG  
 AGCATCTGGGACAGGAGCAGCCGCAATGTCTCAGCTGCTGTGGAAGTTCAGATGCAAGTGGGATGCTCTATGA  
 TCAGGAGGCTGGGACCGCACCTTGGTGAAGGTATCCCCAGGCGAGCTCGGCTCGAGGCGAGTGTGAACCCCA  
 TGCTGCATGAGTACTGCTCAACCATTTGCCACTTGCAGTCAACAACGACACCGGTGAGTACACATGCTGGCA  
 CCTCTGGCCACTGGGACCACTGATGCTGCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
 CGGCTGGGCGCTG  
 TCACCTTCAACTCTGTAGAGGACATAGGCGCGCAGAGTGCCTTCCAGTACTTCCAAAGACCCGAGCCGAG  
 TCCCTCTGCTGAGGCACTGCTCCAAAGGAAGATGCCCTCGAGGAGGACAGGAGCGAGGCGTGGCCAGG  
 CAGGCTGGAGTGTGGGCTCTCTGAGATTTCTAGAGTTGCTCAACAGCCCTGATCAACTAAGTTTTGTGGT  
 ACTTCAACCCTCTTGCCCTCATTTCTGCTGACGAGCATTTGTGAGACTGATGACCAAACTGCACTGGTAAAT  
 TTAGACACTTCTGCTTTTCTGTAATTTGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG  
 TTGGCAGCTGGGCCCCACAGGATGACCAATAAGCCCTTGTGAAGCTGCTTTTAAATGAACACAGAAATTT  
 GGCCACTGTTAAACTCTGCACTCTCACTGTACTTCAATTAATGCCATTAATGAACATATCTTCTCTCTT  
 TTTGCTGATGGTTTGGCCCACTCTGCAATAGTGATAATCTGATGCTGAAGATCAATAAACCATAATAAGCATAT  
 TTTCTGGCCTTGTCTCCAGGACATAGGCAAGCCTTGATCATAGTCTCATACATATTTGGTGAATTTGAGTAAAG  
 AAATAAAAACATATCTTTACTTTGAAATGTAATAACTATTATTTCTTTGTAATTTGTAATTTGTAATTTGTA  
 ACATTCAGGCTTAGCTTAATATATAGGATGCTCTTCTACAGCTCTGGAAGACATCTCCCTGGT  
 ATCCAAATTCACAGGTTGCCAGTGTATTTGTACAAATTTCCCTTGGCATTCGTTTTGTTTCTGCTGTAAGAAC  
 CCAGTGTAGCCAGGCGAGATGTCAATAATGCATACTCTGATTTTCAAAAAA

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPISIFAKPADTLESPEGWTTWFNI  
DYPGGKGDYERLDAIRFYYGDRVCARPLRLAARTDWTGAGSTGQVHVHSGPREGFWCLNREQ  
RPGQNCSNYTVRFLCPGSLRRDTERIWSPWSKSCSAACGQTGVQTRTRICLAEMVSLCS  
EASEBQGHCMGQDCTACDLTCMGGVNADCDACMCQDFMLHGAVSLPGGAPASGAAYLLTK  
TPKLLTQTDSDGFRFIPGLCPDGKSLIKITKVKFAPIVLTMPKTSLKAATIKAEFVRAETPY  
MVMNPETKARRAGQSVSLCCKATGKPRPDKYFWYHNDTLLDPSLYKHESKLVLRKLQHQHAG  
EYFCKAQSDAGAVKSKVAQLIVTASDETPCNPVPESYILRLPHDCFQNCATNSFYDVGRCFV  
KTCAGQQDNIGIRCDVAGNCCGISTGKEETQCSGTYLTPTKVAKESQCRCTETSVNIRGRV  
SADANGEPMRFGHYVMGNSRVMSTGYKTEFTLTHVPQDTERVLTVFDRLQKFTVNTKVLFPN  
KKGSAVFHEIKMLRRKEPITLEAMETNIIPLGEVVGDEPMAELEIPSRSFYRQNGEPIYGKV  
KASVTFLDPRNISTATAAQTDLNFINDEGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHL  
DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKRDRFTVLVGNLEIRERRLFNL  
DVPESRRCFVKVRAIRSERFLPSEQIGGVIVSVINLEPRTGFLSNPRAWGRFDSVITGNGA  
CVPAFCDQSPDAYSAYVLASLAGEELQAVESSKPFNPNAIGVPPQPYLNKLYNRRTDHEDP  
VKKTAFAQISMARRPNSAEESNGPIYAFENLRACEEAPSAHFRFYQIEGDRYDNTVPFN  
EDDPMSWTE DYLAWWPKPMEFRACYIKVKIVGLEVNVRSRNMGGTHRRTVGKLYGIRDVRS  
TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTLKVVI PQGSCRRASVNPMLHEYLVNHLPLAV  
NNDTSEYTM LAPDLPLGHNYGIYITVTDQDPRTAKEIALGRCFDGTS DGSRRMKSNVGVALT  
FNCVERQVGRQSAFQYLQSTPAQSPAAGTVQGRVFSRRQQRASRGGQRQGGVVASLRFPFVA  
OCPLIN



**FIGURE 73**

CTGCAAGTTGTTAAAGCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCCTCAATATACCTGAATACGCAC  
 AATATCTTAACCTCTCATATTTGGTTTTGGGATCTGCTTTGAGTGCCCATCTTCATTTAAAAAAAATACAGAG  
 ACCTACCTACCGGTACGCATACATACATATGTGTATATATATGTAACATAGACAAAGATCGCAGATCATAAAGC  
 AAGCTCTGCTTTAGTTTCCAAAGAGATTACAAAGATTTAGAGATGTTATTTGTCAGATCCCTGTCGATTCATG  
 CCCTTTGGCTTACGGGTCTCCTCAGTGATGCAAGCCCTACCCTTTGGTTTGGGGACATTATGATTTGTGTAAGACT  
 CAGATTTACACGGGAAGAGGGAAGTTTGGGATTACATGGCCTGCCAGCCGGAATCCACGGACATGACAAATTA  
 TCTGAAAGTGAACCTCGATCTCCGGATATTACCTTGGAGACCTTCTTGAGACGTTCTGTGCAATGGGCAAAAT  
 CCTACATGTGCAATAATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCTGAGCTGATGTTTGATTTT  
 GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTGAAGAGATATCCCAAGCCTCTCCAGGTTAAACAT  
 CACTCTGCTTTGGAGCAAAACCATTTGAGCTAACAGACAACTAGTTATTACCTTTGAATCTGGGCTCCAGACC  
 AATGATCTCTGGAGAAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA  
 GATGCTTTTCACATGGATCCTAAATCCGTGAAGGATTTATCACAGCATACGGTCTTTAGAAATCATTTCACAGA  
 AGAGTACTCAACAGGGTATACAACAAATAGCAAAATTAATCACTTTGAAATCAAAGACAGGTTCCGCTTTTGG  
 CTGGACCTCGCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAACCAAGAACTCAGAGATTTCTTT  
 ACAGTCAAGACCTGAGGATAAAGCTGTTAAGACCAGCCGTTGGGGAAATATTTGATAGTGAAGTACACTTGGC  
 ACGTACTTTTACGCGATCTCAGACATAAAGGTGCGAGGAAGTGAAGTGAATCTCCATGCCACTGTATGTG  
 TGTATGACAACAGCAAAATGACATGCAATGTGAGCACAACTACAGGTCAGACTGTGGGAAATGCAAGAAG  
 AATTATCAGGGCCGACCTTGGAGTCCAGGCTCCTATCTCCCATCCCCAAAGGCACTGCAATACCTGTATCCC  
 CAGTATTTCCAGTATTTGGTACGAATGTCTGCGACAACGAGCTCTGCACTGCCAGAACGGAGGACGTCGCCACA  
 ACAACGTCGCTGCTCTGTGCCCGGCCGATACACGGGCATCCTCTGCGAGAAGCTGCGGTGCGAGAGGCTGGC  
 AGCTGCGGCTCGACTCTGGCAGGGGCGCGCCCCGCGACGGCACCCAGCGCTGCTGCTGCTGACCACTGCTGCT  
 GGGAAACGCGCAGCCCCCTGGTGTCTTAGTGTCACTCCAGCCACACCGGACGGGCTGTGCGGTGGGGAAGCA  
 GACACAACCCCAACATTTGCTACTAATAGGAAACACACATACAGACACCCCACTCAGACAGTGTACAAA  
 CTAAGAAGGCTTAACGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGAGTCAAGCTGTTAATTTT  
 TGACTCCAGAGGAGTTGGCAGCTGTGTATATTACTGCAAAATCACATTGCCAGCTGACAGAGCATATTGTGGA  
 TTTGGAAGGCTGCGACAGCCCCCRAACAGGAAGAACAACAAACAAATCAACCGACTAAAAACATTGGC  
 TACTCTAGCGTGGTGGCCCTAGTACGACTCCGCCAGTGTGTGGACCAACAAATAGCATTTCTTGTCTGTGAG  
 GTGCAATTTGGGCTAAGGAATCTGTTACAAGCTGCCATATTGGCCTGCTTCCGTCCCTGAATCCCTTCCAAC  
 CTGGCTTTAGTGAACGTTGCTCTGTAACCCCTCGTTGGTTGAAAGATTTCTTGTCTGATGTTAGTGAAGCA  
 TGTGTAACAGCCCTCTTAAAGCCGCAAGCCAGTATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGGCA  
 GCACATCCCACTATACAAAGAGTGGCTATAGGAAAAAGAAAGTATATCTATCTTTGATTTCAATGAAGTT  
 ATTTTCTTGAACCTACTGTAATATGTAGATTTTGTATTATTGCCAATTTGTGTTACAGACAATCTGTTAAT  
 GTATCTAATTCGAATCAGCAAGACTGACATTTTATTTTGCTCTCTTGGTCTGTTTGTCTTCTGCTGCTGCA  
 GATTTCTCTGTAAGGGCAACAACGCTGCTGGCATCAAGAATATCAGTTTACATATAACCAAGTGAATAAGA  
 TTCCACCAAAAGGACATTTCTAAATGTTTTCTGTTGCTTTTAACTCTGGAAGATTTAAAGATAAAATCTCTGCA  
 TAAACGATTTCCAGAAATTTGATTGCAATTTCTTAAGATTGAAGGAACGCCACCAAGCAGTTTCACTCACT  
 TTAAGTATTTCTGTGGAGCTGAGTCAATTCAGCTGACGAATTTAGTTCCAGGAAGATGGATTGATGTTCACT  
 AGCTTGGACAACTCTGCAAAATATGAGACTATTTCCACTTGGGAAAAATTAACACAGCAAAAAA

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**FIGURE 74**

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK  
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK  
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMLEKSLDYGRWQPYQYYATDCLDAF  
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD  
TTKKLRDFFTVDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN  
SKLTCECEHNTTGPDGCKCKNYQGRPWSPGSYLPPIPKGTANTCIPSISSIGTNVCDNELH  
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTTLLGTAS  
PLVF

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**FIGURE 75**

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGTGGCTAAGATTGCTGAGGAGCGG  
 CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCGCGTCCGGGCGAGGTGTCTCATGACTT  
 CTCTTGTGGACCATGTCCGTGATCTTTTTTGCTGCGTGGTACGGGTAAGGGATGGACTGCC  
 CCTCTCAGCCTCTACTGATTTTTTACCACACCCAAGATTTTTTGGAATGGAGGAGACGGCTCA  
 AGAGTTTAGCCTTGGCAGCTGGCCCAGTATCCAGGTCGAGGTTCTGCAGAAGGTTGTGACTTT  
 AGTATACATTTTTCTTCTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC  
 AGCAGCCATGGCCTTCTGCTTCTGGAGACCCTGTGGTGGGAATTCACAGCTTCTCATGACA  
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTGAG  
 AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGAAAAAAT  
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA  
 ATGGGGTGATGAATGGTCACACCCGATGCACCTTGAGGCTGCTCCTAATTTCCGAATGGAA  
 CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTCTCAACATCATGTGTGCTGCCCTGAATCT  
 CATTCGAGGAGTTACCTTGCAGAACATTCTTACAGGATCCAAGGAGCTGGTTCTGCTGGT  
 TGGACCAAACTCTGTGAGCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT  
 CCGGGAGCAGTGATGTCAAACCTTCTGCTGCTGGGGAAATCTCATCAGCAGGGAGCCTGTGGA  
 AAAGGCATGTCAAGTAAATCTGGGAATGGCTGGATTGCGAAACATCTGCCCATGTGTATTG  
 ATGGCAGAGCTGTGCCCACAAGCGCCTTTATTTAGGGTAAAAATTAACAAATCCATTCTAT  
 TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCCCTTACATTTATATGATTCTGGGGTT  
 GCTTCAGAAGTGTTATTTTCATGAATCATTATATGATTGATCCCCAGGATTCTATTTTGT  
 TTAATGGGCTTTTCTACTAAAGCATAAATACTGAGGCTGATTTAGTCAGGGCAAACCAT  
 TTACTTTACATATTGTTTTTCAATACTTGTGTTTCATGTTACACAAGCTTCTTACGGTTTTTC  
 TTGTAACAATAAATATTTTGTAGTAAATAATGGGTACATTTTAAACAACTCAGTAGTACAACC  
 TAAACTTGTATAAAAGTGTGTAATAATGTATAGCCATTATATCTATGTATAAATTAAATG  
 AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTTTATTAACAAAAAAAAAAAAAAAAA  
 AAAAG

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**FIGURE 76**

MSVIFACVVRVVDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFS IHF  
SSFGDVACMAICSCQCPAAMAFCFLET LWWEFTASYDTTCIGLASRPYAFLEFDS I IQKVW  
HFN YVSSSQMECSLEKIQEELKLQPPAVLTLED TDVANGVMNGHTPMHLEPAPNFRMEPVTA  
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

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**FIGURE 77**

TGCTTCCTGGAGACCCCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT  
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAGAAAGTGAAGTGGCATT  
TTAACTATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGGAAAAAATTCAGGAGGAGCTCAAG  
TTGCAGCCTCCAGCGGTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

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**FIGURE 78**

CTCAGCGGCGCTTCTCGTAGCGAGCCTAGTGGCGGGTGTTTGCATTGAAACGTGAGCGCGA  
 CCCGACCTTAAAGAGTGGGGAGCAAAGGAGGACAGAGCCCTTTAAACGAGGCGGGTGGTG  
 CCTGCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCGAGTT  
 TCTGTGCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGGCGGCGGGCTT  
 CCTCCCCGCTCGTCTCCCCGGGCCAGAGGCACTCGGCTTCACTGCTGAGCAGAGTA  
**TGGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCACGAGAGGATCCGC**  
**GAGTGTATTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCTTGAC**  
**CCGCTTCAAGAAGCTGCTGAGTTACCACAGTGGATGATGAAGATGCCACCGTCAACAAGA**  
**TTGGCGTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGCTGCTGCTGCCCC**  
**TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCCCTCGGAACACTACTACATCCAGTGGCT**  
**CAACGGCTCCCTCATCCATGGCCTCTGGAACCTTGTTTTTCTCTTCCCCAACCTGTCCCTCA**  
**TCCTTCTCATGCCCTTTGCATATTTCTTCACTGAGTCTGAGGGCTTGTGCTGGCTCCAGAAAG**  
**GGTGTCTGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGTCT**  
**AGGTATGGTGTGGGTGGCATCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCT**  
**ATGACTTTTTGGGAGTACTATCTCCCTACCTCTACTCATGCATCTCCTTCTTGGGGTCTG**  
**CTGCTCCTGGTGTGTACTCCACTGGGTCTCGCCCGCATGTTCTCCGTCACTGGGAAGCTGCT**  
**AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAGGAGG**  
**CAGCCCTGACCCGAGGATCTGTAATCCTACTTCCCTGCTGGCTGCTTTAGACATGGAGCTG**  
**CTACACAGACAGGTCTGGCTCTGCAGACACAGAGGGTCTGCTGGAGAAGAGGCGGAAGGC**  
**TTCAGCCTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTGTCTGGTGTGACGG**  
**GCCTGTCTGTGCTCATTGTGGCCATCCACATCCTGGAGCTGCTCATCGATGAGGCTGCCATG**  
**CCCCGAGGCATGACGGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAGCTGGGCTCCTTTGG**  
**TGCCGTCACTCAGGTGTACTCATCTTTTACCTAATGGTGCTCCTCAGTTGTGGGCTTCTATA**  
**GCTCTCCACTCTCCGGAGCCTGCGGCCAGATGGCACGACACTGCCATGACGCAGATAATT**  
**GGGAAGTGTGTCTGCTCCTGGTCTTAAGCTCAGCACTTCTGTCTTCTCTCGAACCTTGGG**  
**GCTCACTCGCTTTGACCTGCTGGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACA**  
**TTGTGTCTCTACAAACGAGCCTTTGACAGGCTCACCACTCTGTCTGGTGAAGACCTTC**  
**ACTGCAGCTGTGCGGCGAGAGCTGATCCGGGCCCTTTGGGCTGGACAGACTGCCGCTGCCCGT**  
**CTCCGGTTTCCCCAGGCATCTAGGAAGACCCAGCACAGTGA****CTCCAGCTGGGGTGGGA**  
**AGGAAAAA****CTGGACACTGCCATCTGCTGCCTAGGCTGGAGGGAAGCCCAAGGCTACTTGG**  
**ACCTCAGGACCTGGAATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGAGCCATCTGCATAATT**  
**GCATAATCTGAGCCAGAGTTTGGGACCAGGACCTCCTGCTTTTCCATACTTAACTGTGGCCT**  
**CAGCATGGGTTAGGCTGGGTGACTGGGTGATGCCCTGATCCCAATCTGTTTACACATCA**  
**ATCTGCCCTACTGCTGTCTGGGCCATCCCCATAGCCATGTTTACATGATTTGATGTGCAAT**  
**AGGTTGGGTTAGGGGAGGGAAGGACTGGGCCAGGGCAGGCTCGGGAGATAGATTGTCTCC**  
**CTTGCCCTTGCCCGCAGCAGAGCCTAAGCACTGTGCTATCCTGGAGGGGCTTTGGACCACTTC**  
**AAAGACCAAGGGATAGGAGGAGGAGGCTTCA****GCATCAGCAATAAAGTTGATCCCAGGGA**  
 AAAAAA

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**FIGURE 79**

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDATVNK  
IALELCTFTLAIALGAVLLLLPFSIISNEVLLSLPRNYIQLNGSLIHGLWNLVFLFPNLSL  
IFLMPFAYFFTESEGFAGSRKGVLRVYETVVMLMLTLLVLGMVWVASAIVDKNKANRESL  
YDFWEYYLPYLYSCISFLGVLLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEEQLYCSAFEE  
AALTRRICNPTSCWLPLDMELLHRQVLALQTQRVLLEKRRKASAWQRNLGYPLAMLCLLVLT  
GLSVLIVAIHILELLIDEAAMPQGTSLGQVSFSKLGSGFAVIQVVLIIFYLMVSSVVGFY  
SSPLFRSLRPRWHDAMTQIIIGNCVCLLVSSALPVFSRTLGLTRFDLLGDFGRFNWLGNFY  
IVFLYNAAFAGLTTLCLVKTFATAAVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ

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**FIGURE 80**

GGCTGCCGAGGGAAGGCCCTTGGGTTGGTCTTGTTGCTTGCGGCGGCGGNTTCNTCCCC  
GCTCGTCCTCCCCGGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC  
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCACGAGAGGATCCGCGAGTGTA  
TTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC  
AAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCG

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**FIGURE 81**

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAACGAGGCGGTGGTGC  
CTGCCCTTTAAGGGCGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCGAGTTTC  
TGTCGCAGGCTGCGAGGAAAGCCCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGCGGCTTCCT  
CCCCGTTGTCNTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA  
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT  
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC  
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC  
GCTCGAGCTGTGCACCTTTACCCCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCCCTTCT  
CCATCATCAGCAATGAGGTGCTGCACTCCC

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**FIGURE 82**

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT  
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTT**CATG**CTGCTGT  
GGGTGATATTACTGGTCCTGGCTCCTGTGAGTGACAGTTTGCAAGGACACCCAGGCCATT  
ATTTTCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCCTCACTTGCAA  
GGGATTCGCTTCTACTCACCACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA  
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTGAGGAATCTGGAGAGTACAGATGCCAG  
GCCCAGGGCTCCCTCTCAGTAGCCCTGTGCACTTGGATTTTTCTTCAGAGATGGGATTTCC  
TCATGCTGCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACC**TAG**GCCTCTC  
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC  
TCTGTGGTTCTGAGGTGCCGGGCAAAGGCGGAAGTAACACTGAATAATACTATTTACAAGAA  
TGATAATGTCTGTCATTCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA  
AAA

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**FIGURE 83**

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHRYL  
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDFSSEMGFPHAAQANVELLGSSDLLT

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**FIGURE 84**

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCGGTTGT  
 GAGGCGGCCCTCACAGGGCCGGGTGGGCTGCGGAGCCGACGCGGCGGCGGAGGAGGCTGTGAG  
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAACCATGGGCTCCGCAGAACTGAGCACCTTTT  
 GCCTGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGACGAGATTTCTATAAGATCTTG  
 GGGTGCCTCGAAGTGCCTCTATAAAGGATATTAAAAAGGCCTATAGGAACTAGCCCTGCA  
 GCTTCATCCCGACCGGAACCCCTGATGATCCACAAGCCAGGAGAAATTCAGGATCTGGGTG  
 CTGCTTATGAGGTTCTGTGAGATAGTGAGAAACGAAACAGTACGATACTTATGGTGAAGAA  
 GGATTAAAAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTCACACTTCTTTGGGGATTT  
 TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATCCAAGAGGAAGTGATA  
 TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT  
 AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTCGGCAAGAGAT  
 GCGGACCACCCAGCTGGGCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT  
 GCCCTAATGTCAAACCTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG  
 AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG  
 AGATTTACGGTTCGGAATCAAAGTTGTCAAGCACCCAAATATTTGAAAGGAGAGGAGATGATT  
 TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT  
 CACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCT  
 ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA  
 TCACCTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA  
 CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTG  
 AATAAAATTGGACTTTGTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT  
 TTGTGTGTGTTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTTATCTAATGA  
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTTGCATTGCGAAAAGAATGACC  
 AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGTGCCGCCCTGAGT  
 TTCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA  
 GTTGTGTAGCAATTCATTCAAATGCCAAGTGGAGAAGTCTGTTTTTAAATACATTTTGTTG  
 TTATTTTTTA

**FIGURE 85**

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKALQLHPDRNPDDPQ  
 AQEKFQDLGAAEVLSDSEKRRQYDTYGEGLKDGHQSSHGDI FSHFFGDFGFMFGGTPRQQ  
 DRNI PRGSDIIVDLVTLLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ  
 MTQEVVVCDECPNVKLVNEERTLEVEIEPGVRDGMETPFIFIGEGEPHVDGEPGDLRFRIKVVKH  
 PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGLPNFD  
 NNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNLQGY

**Important features:****Signal peptide:**

amino acids 1-22

**Cell attachment sequence.**

amino acids 254-257

**Nt-dnaJ domain signature.**

amino acids 67-87

**Homologous region to Nt-dnaJ domain proteins.**

amino acids 26-58

**N-glycosylation site.**

amino acids 5-9, 261-265

**Tyrosine kinase phosphorylation site.**

amino acids 253-260

**N-myristoylation site.**

amino acids 18-24, 31-37, 93-99, 215-221

**Amidation site.**

amino acids 164-168

**FIGURE 86**

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA  
GCGGCGGGCGGAGGAGGTTTTGAGGATTTTGGAAACAGGACCCGGACAGAGGAACCATGGTT  
CCGCAGAACNTGAGCACNTTTTGCTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG  
ACGAGATTTNTATAAGATTTTGGGGTGCCTNGAAGTGCCTTNTATAAAGGATATTAAGG  
CCTATAGGAACTAGCCCTGCAGNTTATCCCGACCGGAACCTGATGATCCACAAGCCCAG  
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGGAAACA  
GTACGATAATTATGGTGAAGAAGGATTAAGATGGTNATCAGAGCTCCCATGGAGACATTT  
TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA  
AATATTCCAAGAG

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**FIGURE 87**

GGCACGAGGCGGGCGGGCAGTCGCGGGATGCGCCCGGGAGCCACAGCCTGAGGCCCTCAGGT  
 CTCTGCAGGTGTCTGTGGAGAACTAGCACCTGCCATCCTCTTCCCCAATTTGCCACTTCCA  
 GCAGCTTTAGCCCATGAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAGCATGG  
 AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGCAGCC  
 TTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTC  
 TAAGCCCATTTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC  
 TGGACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC  
 GAAGATGCCTCGGGTCTCATGTCCACTGCATTGCCATCTTGAAGATTTGTACACTCTGAC  
 AGAGAAGCTTGTGCCATGACAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA  
 GCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG  
 TACCCTCCGTTGGACCCCAAACCTCCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTGAC  
 TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCTGGACTGGATTGACC  
 AGTCTCTGTGGCTGCTGAGGAGCATTTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG  
 CCAGATAAAGGCCTCCGAGGCCCTGAAGGCTTCTGACGAGCAGTCTGCAATTTAGTGCCT  
 ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCGGCCATCCCTGGATGGCTCAGCTTAGCCTT  
 CTACTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTCATAG  
 TAAAGCAGGAGATCCCCGTCAGTTTATGCCTCTTTTGCAGTTGCAAACTGTGGCTGGTGAGT  
 GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAA  
 CTGGTGGACTGTGAGCTTTATTAGCTACCTAGTGTTTTCAAGAAAAATTGAGCCACCGTCT  
 AAGAAATCAAGAGGTTTACATTAAATTAGAATTTCTGGCCTCTCTCGATCGGTGAGAATG  
 TGTGGCAATTCTGATCTGCATTTTTCAGAAGAGGACAATCAATTGAAACTAAGTAGGGGTTTC  
 TTCTTTTGGCAAGACTTGTACTCTCTCACCTGGCCTGTTTCATTTATTTGTATTATCTGCCT  
 GGTCCCTGAGGCGCTCGGGTCTCCTCTCCCTTGACAGGTTTGGGTTTGAAGCTGAGGAAC  
 ACAAGTTGATGATTCTTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG  
 GATAGTAAATTTATACTTATGTTCCCTCAAAAAAAAAAAAAA

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**FIGURE 88**

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSEL  
ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKT SAS  
VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTALLLSVSHLVLVTRNACHLTGGLDWI  
DQSLSAEEHLEVLREALASEPDKGLPGPEGFLQEQSAI

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GCCTCATTTCTCCGACTCAGCTTCCACCCCTGGGCTTTCGAGGTGCTTTCGCCGTGTCC  
CCACCACTGCAGCCATGATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA  
TTTGGAGTGTTTTCTGTCTTTGGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT  
TGAAATGTTTTATTGTAGCCGGCTTGGCTTTTGTAATTGGTTTAGAAAGAACATTAGAT  
TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTCTGGTGGTGTATTGTAGTC  
CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTCTCTGTTCAG  
GGGCTTCTTCTGTGCTGTTGTGGCTTTATTAGAAGAGTGCCAGTCCTTGATCCCTCCTAAAT  
TTACCTGGAATTAGATCATTTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATTAACA  
AGTGAATTTGAAGACTCATTTAAATATTGTGTTATTTATAAAGTCATTTGAAGAATATTC  
GCACAAAATTAAATTACATGAAATAGCTTGTAAATGTTCTTTACAGGAGTTTAAACGTATAG  
CCTACAAAGTACCAGCAGCAAAATTAGCAAAGAAGCAGTAAACAGGCTTCTACTCAAGTGA  
ACTAAGAAGAAGTCAGCAAGCAAACCTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA  
ACTCTGAAGGCTATTGTGTGTTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA  
CTGTGGTGCTGTTTCTTTCTTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT  
TTTTAGAAGTGTCCACTGCAATGGCAAAAATATTTCAGTTGCATGTATCTCTGGAAGTGA  
TGCATGAATTGCAATTGGATTGTGTCATTTTAAAGTATTAAAACCAAGGAAACCCCAATTTG  
ATGTATGGATTACTTTTTTTGNGNCAGGGCC

## FIGURE 90

MSISLTDQKIGMGLTGFVVFLLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTRFRFFQK  
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVLGSLNLNLPGI  
RSFVDKVGESNNMV

### Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

**FIGURE 91**

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTTCTCCCGACTCAGCTTCCC  
ACCNTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCCCCACCACTGCAGCCATGATCTCCTTAA  
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTGGAGTGTTTTCTCTTCTTTGGA  
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGAAAATGTTTTATTTGTAGCCGGCTT  
GGCTTTTGTAATTGGTTTAGAAAGAACATTGAGATTCTTCTTCCAAAACATAAAATGAAAG  
CTACAGGTTTTTTCTGGGTGGTGTATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATG  
ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

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**FIGURE 92**

GGCAGGAGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA  
GGCTGCCAGGAAGGAGACGCCCTTCCTGAGTCCTGGATCTTTCTTCCCTTCGGAAATCTTTGA  
CTGTGGGTAGTTATTATTCTGAATAAGAGCGTCCACGCATCATGGACCTCGCGGGACTGC  
TGAAGTCTCAGTTCCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATC  
ATCAACACCATTAGCTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCCGGAA  
GATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT  
CGGGCACGGAATGCACCATCTTCACGGACCCGCGCGCCTACCTCAAGTATGGGAAGGAAAAT  
GCCATCGTGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA  
ACGCTTTGGGCTGTTAGGGGGCTCCAAGGTCCTGGCCAGAAAGAGCTGGCCTATGTCCCAA  
TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTGCGCAAGTGGGAGCAGGAT  
CGCAAGACGGTTGCCACCAGTTTGCAGCACCTCCGGGACTACCCCGAGAAGTATTTTTTCTCT  
GATTCACTGTGAGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC  
GGCCAAAGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC  
ACCGTGAGGAGCTTGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTCAGAAA  
TAATGAAAATCCAACACTGCTGGGAGTCTAAACGGAAAGAAATACCATGCAGATTTGTATG  
TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCAC  
AAGCTCTACAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGACCTTCCCAGA  
GACGCCCATGGTGCCCCCCCCGGCGGCCCTGGACCCCTCGTGAAGTGGTGTGTTTGGGCTCGC  
TGGTGCTCTACCCCTTCTTCCAGTTCCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACG  
CTGGCCAGCTTCATCCTCGTCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT  
GACGGAATTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT  
GACTCAGGGAGGTGTACCATCCGAAGGGAACCTTGGGGAACCTGGTGGCCTCTGCATATCCT  
CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCTGCTGGGCACGGCGGAAGTCACGA  
CCTCTCCAGCCAGGGAGTCTGGTCTCAAGGCCGATGGGAGGAAGATGTTTTGTAATCTTT  
TTTTCCCATGTGCTTTAGTGGGCTTTGGTTTTCTTTTGTGCGAGTGTGTGTGAGAATGGC  
TGTTGTGTGAGTGTGAACTTGTCTGTGATCATAGAAAGGTATTTTAGGCTGCAGGGGAG  
GGCAGGGCTGGGGACCGAAGGGGACAAGTTCCTTTTCATCCTTTGGTGTGAGTTTTCTGT  
AACCCTTGGTTGCCAGAGATAAAGTGAAAGTGCTTTAGGTGAGATGACTAAATTATGCCTC  
CAAGAAAAAAAATTAAGTGCTTTTCTGGTGCAAAAAAAAAA

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**FIGURE 93**

MDLAGLLKSQFLCHLVFCYVFIFASGLIINTIQLFTHLLWPINKQLFRKINCRLSYCISSQLV  
MLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHNKFEIDFLCGWSLSERFGLLGSKVLAKK  
ELAYVPIIGWMWYFTEMVFCSRKWEQDRKTVATSLQHLRDYPEKYFFLIHCEGTRFTEKKHE  
ISMQVARAKGLPRLKHLLPRTKGFAITVRSLRNVVSAVYDCTLNFRNNENPTLLGVNLGKK  
YHADLYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTFPETPMVPPRPWTLVN  
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVWRMMIGVTEIDKGSAYGNSDS  
KQKLND

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CTGAGCGCGCGGTAGC**ATG**GAGGGGGAGAGTACGTGGCGGTGCTCTCGGGCTTTGTGCTCGCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAA GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTCCAAATGGATGATGTTGAAGTTGTTTA TACAATTGACATTCAGAAATATATTCCATGCTATCAGCTTTTACGCTTTTATAATTCTTCAG GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTTATCAAATGTCAAAAGAGATGTGGTAGGT TGGTACAAATTCGTCGTCATTTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA AAACCTTGCAGGAGCATTTTTTCAAACCAAGACCTTGTTTTTCTGCTATTAAACCAAGTATAA TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTT TTTTCACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGTCTGAACAACTGGGTTATAAAAC TGTATCAGGTTCTGTATGTCCTACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT TTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAAATGAAATGSTATGCTTCATTA CAAGAGGAATTAAGAGTATATGCAAAAAAGTGAAGACAGTGAACAGCAGCAGATATAAACT AGTAAAGGATGTAAACAGATATAAACGAGAAATTTAGAGAAAGAGAGGAGCAGATTCAGG CACAAGAGAGAAACATCCAAAAAGACCTTCAGGAGAACATTTTTCTTTGTTCAGGCATTA CGGACCTTTTTTCCAATTTCTGAATTTCTTCATTCATGTGTTATGTCTTTAAAAAATAGACA TGTTTCTAAAAAGTAGCTGTAACACACCACCATCTCGATGTAGTAGACAATCTGACCTTAA TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAAGCAT AAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGGTTGTTAGATACACAAGA CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAATGAGCAGCC CAGAAACAGATGAAGAAATTTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCCTTACA TTTTGAATCCTTTTAACTTACAGGAGATTTTTTTATTTFGGCTGATGGGTAAAGCCAAACAT TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTTCATTTGTTTTTACTATGTTTAC CTGTTTGCAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAAC ATCAGATGCTTTTATTTCCAAACCTTTTTTTTACCTTTTCACTAAGTTGTTGAGGGGAAGGCT TACACAGACACATTCTTTAGAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAA TCCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC TGGGCAACGTATTGAGACCATGTCTATTAATAAATAAAATGGAAAGCAGAAATAGCCTTAT TTTCAAAATATGGAAAGAAATTTATATGAAATTTATCTGAGTCAATTAAAGATTTCTCCTTAAG TGATACTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATATAAATGCTGGATATCATGCA ATAAATTTGCAAAACATCATCTTAAATTTAAAAAATAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 95**

MEGESTSAVLSGFVLGALAFQHLNTSDTEGFLLGEVKGEAKNSITDSQMDDVEVVYTIDIQ  
KYIPCYQLFSFYNSSGEVNEQALKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEH  
FSNQDLVFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSC  
MSTGFSRAVQTHSSKFFFEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN  
RLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSS  
CNYNHLDVVDNLTLMVEHTDIPEASPASTPQIIKHKALDLDNRWQFKRSRLDQDKRSKA  
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTF

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**FIGURE 96**

GGCACAGCCGCGCGCGGAGGCGCAGAGTCAAGCCGAGCCGAGTCCAGCCGAGCAGAGCGGACCAGCGCAGGGCCAGC  
 CCAAGCAGCGCGCGCAGGAAACGCCGCCGCCGCCACACCCCTCTGCGGTCGCCCGCGCGGCTGCCACCCCTCCCT  
 CCTTCCCCCGCTCCCCGCTCGCCGGCCAGTCAGCTTGCCGGGTTTCGCTGCCCCGCGAAACCCCGAGGTACACCA  
 CGCCCGGCCCTCTGCTTCCCTGGGCGCGCGGCCGCCCTCCACGCCCTCCTTCTCCCTGGCCCGCGCGCTGGCAC  
 GGGGACCGTTTCTGACCGCGAGGCCCGAGCTCTACTTTTCGCCCGCGCTTCTCCGCTGCTCGCCTCTTCCAC  
 CAAC<sup>T</sup>CCAAC<sup>T</sup>CTCTCTCCCTCCAGCTCCACTCGCTAGTCCCCGACTCCGCGCAGCCCTCGGCCGCTGCCCTAG  
 CGCCGCTTCCCGCTCCGCTCCAAAGTGGGAACGCTCCGCCCGCGCCGCA<sup>ATG</sup>CGACGCTTCGGCTTGC  
 CGCGCTTCTGCAACCCCTGGCAGTGTCTCAGCGCCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGG  
 AAGTGCAGCTCTTTACGTGTCTCAAAGGCTTCAACAAGAACGATGCCCCCTCCACGAGATCAACGGTGATCAT  
 TTGAAGATCTGTCCCAGGGTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAAGTAAAGA  
 TGATTCAAAGTGTGGTCAGCGAACAGTGCATCATTTGCAAGCTGTCTTTGCTTCAAGTTACAAGAAGTTTG  
 ATGAATCTTCAAAGAAGTACTTTGAAAATGCAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGGCCAT  
 TTATACATGCAAAATCTGAGCTATTAAAGATCTCTTCTGAGATTGAAACGTTACTACGTGGTGGGAAATGT  
 GAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTTCCGCTGGTGAACCTCCAGT  
 ACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCT  
 CGCAAAATTGAAGCTCCAGTTACTCGTCTTTGTAGCAGCCCGTACTTTCGCTCAAGGCTTAGCGGTTGCGGG  
 AGATGTCGTGAGCAAGTCTCCGTGGTAAACCCACAGCCCAAGTGTACCCATGCCCTGTTGAAGATGATCTACT  
 GCTCCCCTGCCGGGCTCTCGTGA<sup>T</sup>GTGAAGCCATGTTACA<sup>ACT</sup>ACTGCTCAAA<sup>AT</sup>CATGAGAGGCTGTTTG  
 GCCAACCAAGGGGATCTCGATTTTGAATGGAACAAATTTATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA  
 GGGTCTTTCAACATTGAATCGGTATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGG  
 ATAATAGTGTCAAGTGTCTCAGAAGGTTTCCAGGGATGTGGACCCCCCAAGCCCTCCACGCTGGACGAAT  
 TCTCGTTCCTCTCTGAAGTGCCTTCAGTGTCTGCTTCAGACCACATCACCCCGAGGAACGCCCAACCAAGCAGC  
 AGCTGGCACTAGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATTTCTGGTCCG  
 CCCTTCGAGCAACGTTTGAACGATGAGAGATGGCTGCAGGAACGCCAATGAGGATGACTTTTGAATGGG  
 AAAGGCAAAAGCAGGTACTCTTTTTCAGTGACAGGAAATGGAATAGCCAACCAAGGCAACACCCAGAGGTTCCA  
 GGTTGACACCAAGCAACACAGACATCTGATCCTTCGTCAAATCATGGCTTTCGAGTGA<sup>T</sup>GACCAAGATGA  
 AGAATGATACAAATGGGAACGACCTGGACTTCTTGATATCAGTGA<sup>T</sup>GAAGTAGTGGGAAGAAAGTGGAAATG  
 GGCTGTGAGTATCAGCAGTGCCTTCAGAGTTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGA  
 GAAAGCGCAGTGTGGTGTCCGCTCGGGCAGCGCTACCTCCTCACTGTCTCTGCATCTTGTCTCTGG  
 TTATCAAGAGAGTGGAGAT<sup>TAA</sup>TTCTCAA<sup>ACT</sup>CTGAGAAAAGTGTTCATCAAAAGTTAAAGGCACCAAT  
 ATCACTTTTCTACCATCTCTAGTGA<sup>CT</sup>TTGCTTTTAAATGAATGGCAACAATGTACAGTTTCTTACTATGGC  
 CACTGGTTTAAAGAGTGTGACTTTGTTTCTCATTCAGTTTGGAGGAAGGAGCTGTGCATTGAGTTGGT  
 TCCTGCTCCCCCAACCATGTTAAAGTGGCTAACAGTGTAGGTACAGA<sup>ACT</sup>ATCTAGTTCTGCA<sup>TT</sup>TTGTGA  
 TTTTATCACTCTATTATTTGTTGTATGTTTTTCTCATTTTGGTTTGGGTTTCTTTTCCA<sup>CT</sup>GTGATCT  
 CGCCTTGTCTTCAAGCAAAACAGGGTCCCTCTTGGCAGTAAACATGTACGATTTCTGAAATATTAAATA  
 GCTGTACAGAGCAGGTTTATTATCATGTTATCTTATTAAAGAAAAGGCCCAAAAGC

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**FIGURE 97**

MARFGLPALICTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ  
GSTCCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF  
VKTYGHLYMQNSSELFKDLFVELKRYVVGNVNLEEMLNDFWARLLERMFLVNSQYHFTDEY  
LECVSKYTEQLKPFQDVPRKLLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL  
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLD FEWN NFIDAMLMVAERLEGPFNIES  
VMDPIDVKISDAIMNMQDNSVQVSQKVFQCGPPKPLPAGRISRISSESASFARFRPHHPEE  
RPTTAAGTSLDRLVTDVKEKLQAKKFWSSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYL  
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDIDESSGE  
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

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**FIGURE 98**

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT  
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA  
GCAACTTACAGCTGCACCGACAGTTGCGGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGC  
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCAC  
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA  
AGATTGGTTTCTGAGAGCCCCGAGAAGAAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGC  
AGTGCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGA  
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT  
TGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTAACATTCTCAGCCAAGAA  
GACAGTGAGCACACCTACCAGACACTCTTCTTCTCCACCTCACTCTCCCACTGTACCCACC  
CCTAAATCATTCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTGTTGTTGCTCTC  
TCTAGTGCTTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCAGGCTTAGGCTT  
AATTACCTGAAAGATTCCAGGAACTGTAGCTTCTAGCTAGTGTGCTATTTAACCTTAAATGC  
AATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTTAAATGTCAAAAAAAAAAAAAAAAAA

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**FIGURE 99**

MKVLISLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR  
KFMTVSGLPKKQCPDHFKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCTCTGGGACTGCTTGTCTTATTCTTGACCT  
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA  
AAGCCAGACTTCCCCAAATTCTTAAGCCTCTGGGCACAGAGATCATTGAGAATGCAGTCGA  
GTTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA  
AACATTTCATCAAAGTGAATCCTCAGGACACACCCATGTGGCTCTGGACAATCCAAGAGCA  
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC  
TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAAACAGAACTCATTTTGAACACC  
CTGACTGCATTTTGTCTTTTAGAAAGTTAGAATAAAATATGGCGCTTTGGGATCACATAGTTG  
ATGGAGAGGAAAAA

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**FIGURE 101**

MAVLVLRLTVVLGLLVLF LTCYADDKPKPKDDKPDGSKDPKPDFPKFLSLLGTEI IENAVE  
FILRSMRSTGFMEDDNEGKHSSK

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**FIGURE 102**

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT  
 CAGAGCTGGTCTGCC**ATG**GACATCCTGGTCCCCTCCTGCAGCTGCTGGTGTCTTCTTAC  
 CCTGCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCGTGTGCAAAAGCTACTTCC  
 CCTACCTGATGGCCGTCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG  
 CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGG  
 CTGCGGAACCGGAGCCAACTTTCAGTTCTACCCACCGGGCTGCAGGTCACCTGCCTAGACC  
 CAAATCCCCACTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT  
 GAGCGGTTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT  
 GGTGGTCTGCACTCTGGTGTGTGCTCTGTGCAGAGCCCAAGGAAGTCTGCAGGAGGTCC  
 GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTCTGGGAGCATGTGGCAGAACCATATGGA  
 AGCTGGGCCTTCATGTGGCAGCAAGTTTTCGAGCCCACCTGGAACACATTGGGGATGGCTG  
 CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAAATGG  
 AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC  
 AAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAACA  
 AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACC**TAG**CAGAATGAGAGAAGACATT  
 CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC  
 CCGCCTTCGACAGTGA AAAAGCTCTACTTCTACGCTGACCCAGGGAGGAACACTAGGACCC  
 TGTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCCTCCCAATGTTGTC  
 CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGT  
 CTCTAGGAAGTGGTCACAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCCTCT  
 CTCCCCACTACCACCTTCTTCTGAGCTGGGGGACACAGGGAGAATCAGAGATGCTGGGGAT  
 GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGA  
 AACCACG

099043-11501

**FIGURE 103**

MDILVPLLQLLVLLLTPLPHLMALLGCWQPLCKSYFFPYLMAVLTPKSNRKMESKKRELFSQI  
KGLTGASGKVALLELGC GTGANFQFYPPGCRVTC LDPNPHFEKFLT KSMAENRHLQYERFVV  
APGEDMRQLADGSMDVVVCTLVLC SVQSPRKVLQEVRRVLRPGGV LFFWEHVAE PYGSWAFM  
WQQVFEPTWKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWL PVGPHIMGKAVKQSFP  
SSKALICSFPSLQLEQATHQPIY LPLRGT

GTGGGATTATTATTAGAGTGAAGATCGTTTTCTCAGTGGTGGTGAAGTTGCCTCATCGCAG  
CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAG  
ACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAAGTAAACATCATCATCTTGG  
TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCCTCAGCTTGAGCAGTTTG  
TTAAGGAATGAGGTTACAGATTGAGGAATTGTAGGGCTCAACCTATAGACTTTGTCCCAA  
TGCTCTCCGACATGCAGTAGATGGGAGACAGAGGAGATTCTGTGGTCATCGCTGCATCTG  
AAGACAGGCTTGGGGGGGCCATTGACGCTATAAACAGCATTGACGACAACACTCGCTCCAAT  
GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCTGGCTCAACAG  
TGATTCCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCCTAAACTTTTGAAGGAA  
AAGTAAAGGAGGATCTTGACCAGGGGGAATCCATGAACCTTTAACCTTTGCAAGGTTCTAC  
TTGCCAATTTCTGGTTCACAGCGCAAGAAGGCCATATACATGGATGATGATGTAATTTGCA  
AGGTGATATTTCTGGCCCTTTACAATACAGCAGTGAAGCCAGAGCATGCAGCTGCATTTTCAG  
AAGATTGTGATTCACGCTCTACTAAGTTGTTCATCCGTGGAGCAGGAACCAGTACAATTAC  
ATTGGCTATCTTGACTATAAAAAGGAAAGAATTGTAAGCTTTCCATGAAAGCCAGCACTTG  
CTCATTTAATCCTGGAGTTTTTGTTCGAAACCTGACGGAATGGAACGACAGAATATAACTA  
ACCAACTGGA AAAATGGATGAAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCTTGCT  
GGTAGCATCACACACCTCCTCTGCTTATCGATTTTATCAACGCACTCTACCATCGATCC  
TATGTGGAATGTCGCCACCTTGGTTCAGTGCTGGA AACGATATTCACCTCAGTTTGTA  
AGGCTGCCAAGTTACTCCATTGGAATGACATTTGAAGCCATGGGGAAGGACTGCTTCATAT  
ACTGATGTTTGGGAAAAATGGTATATTCCAGACCCAACAGGCAAAATCAACCTAATCCGAAG  
ATATACCGAGATCTCAAACATAAAGTGAACAGAAATTTGAAGTGAAGCAAGCATTCTCTCAG  
GAAGTCTTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA  
GCAAGCCATGGA AAAAGATGTGTCAGCTAGGTAAGATGACAACTGCCCTGTCTGGCAGTC  
AGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTTTTCTT  
ACTACAATGCTGAATGACTGGAAGAAGAACTGATATGGCTAGTTTCAGTACGCTGTGTACAGA  
TAATTCAAAACCTGCTGTTGGTTTTAATTTTGAACCTGTGGCCTGATCTGTAATAAACTT  
ACATTTTTC



**FIGURE 105**

MSFRKVNIIILVLAVALFLLVLHHNFLSLSSLLRNEVTD SGIVGPQPIDFVPNALRHAVDGR  
QEEIPVVIAASEDRLGGAIAAINSIOHNTRSNVIFYIVTLNNTADHLRSWLNDSLKSIRYK  
IVNFDPKLLEGKVKEPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT  
ALKPGHAAAFSEDCDSASTKVVIRGAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA  
NLTEWKRONITNQLEKWMKLNVEEGLYSRTL AGSITTPLLIVFYQQHSTIDPMWNVRHLGS  
SAGKRYSPQFVKA AKLLHWNHGLKFWGRTASYTDVWEKWYIPDPTGKFENLIRRYTEISNIK

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**FIGURE 106**

TGGTTTTTGCCCCATAAATCCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT  
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT  
GGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT  
TGCAGCTATAAACAGCATTAGCACAACACTCGNTCCAATGTGATTTTCTACATTGTTACTC  
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA  
TACAAAATTGTCAATTTTGACCCTAAACTTTTGGAAGGAAAAGTAAAGGAGGATCCTGACCA  
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCCAGCG  
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC  
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTAGCCTCTAC  
TAAAGTTGTCATCCGTGGAGCAGGAAA

**FIGURE 107**

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG  
 GAGCTAGAGGGCAAGTGTGCTCGGCCACGCTGCAGGGAACGCGGGCGGCCAGACAACGGGC  
 TGGGCTCCGGGGCTGCGGCGCGGGCGCTGAGCTGGCAGGCGGGTTCGGGCGCGGGCTGCA  
 TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGCCGCGGCGAGCCTTTGAGGGGAACGACT  
 TGTGCGAGCCCTAACGAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGAGCGTCACATCACT  
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCACT  
 CCGTAAAGTAAACATCATCATCTTGGTCTGGGCTGTTGCTCTCTTCTTACTGGTTTTGCAC  
 CATAACTTCCTCAGCTTGAGGCAGTTTGTAAAGGAATGAGGTTACAGATTGAGGAATTGTAG  
 GGCCTCAACCTATAGGACTTTGTCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA  
 GGAGATTCTGTGCTCATCGCTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAA  
 ACAGCATTCAGCACAACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATTACA  
 GCAGACCATCTCCGGTCCTGGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAATTG  
 TCAATTTTGACCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCC  
 ATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGGTTCCCAGCGCAAGAAGG  
 CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCA  
 CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTGAGCCTCTACTAAAGTTGT  
 CATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA  
 TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAAC  
 CTGACGGAATGGAACGACAGAATATAACTAACCAACTGAAAAATGGATGAACTCAATGT  
 AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCG  
 TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCAGT  
 GCTGGAACACGATATTACCTCAGTTTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACA  
 TTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGAAAAATGGTATATTTCCA  
 GACCCAACAGGCAAATTAACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAAG  
 CAGATTTGAACTGTAAGCAAGCATTCTCAGGAAGTCCGGAAGATAGCATGCGTGGGAAG  
 TAAAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAAGAAAGATGTGTGAGTAG  
 GTAAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCAGACAGACTATAGACTATAAAT  
 ATGTCTCCATCTGCCTTACCAAGTGTCTTCTTACTACAATGCTGAATGACTGGAAAGAAGAA  
 CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAACTGCTGTTGGTTTTAATTTT  
 GTAACCTGTGGCTGATCTGTAATAAACTTACATTTTCAATAGGTAAAAAAAAAAAAA  
 AAAAAA

CTGCAGGTAGACATCTCCACTGCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT  
GAAGCCGGCCATACCAGAGTCTGCCTCGGCATGGGCCCTACCATTGAGGCAGCTCCACTG  
TCTGTGCTGGTCTGAGGGTGTCTGCCTGTCTATGGGGGCAGCCATCTCCCAGGGGGCCCTCATC  
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTCTGGGTTCATCCTCTGCTG  
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTGTAATCCAGTCCCAACTCCAGCCC  
TGGCCCTCTGCTCTGAGAAAGGCCCCACCACCCAGAAAGCCAGGCATGAAGGCAGTACCTGC  
TGCAGCCCTGAAGGCCCTTGGCTAGCCTGGAGCCAGGACCTTAAGTCCACCTCACCCTAGAG  
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT  
TGGAGCTGGACCCAGCGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC  
TAAGGAGATGGGCCTGGGGTGGGGGCTTATGAGTTGGTGCTAGAGCCAGGGCCATCTGGACT  
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTCCCTAGGCTGAGCACC  
TCTAGGCCCTCTAGGTTGGGGAAGCAAATGGAACCCATGGCAATAATAGGAGGGTGTCCAG  
CTGGGCCCTCTCCCTGGTCTCCAGTGTCTGCTGGATAATAAATGGAATATGGCTCTAA  
AAAAAAAAAAAAAAAAAA

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**FIGURE 109**

MGAAISQGALIAIVCNGLVGFLLLLLVILCWACHSRLPTLTLSLNPVPTPALAPVLRPHH  
PRSPAMKAATCCSPEGPWPSLEPRT

0990047.11100  
109111.12100660

**FIGURE 110**

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCAGGCTACCA  
 GTTCCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA  
 CTCCTTATTTGCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCCTAAGTGGAA  
 TC**CATG**TCGGGAAGAGATAACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGCTCTTTGGCC  
 ATGATGTTTACCTTCAGATTATCACCACCCTTCTGGTTCACATTTTCATTTTCATTGGTTAT  
 TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC  
 TCAGCATAGAATTGGACACAGAAAGGAAAAATGAAGTGCGTGCTGGGGTTTGCTATCGTA  
 TCCACAGGCATCACGGCAGTGCTGCTCGTCTTGATTTTTGTCTCAGAAAGAGATAAAAT  
 GACAGTTGAGCTTTTCCAAATCACAAATAAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCC  
 AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTG  
 AGCCTGGGAACATGCAGGAGCTGCCAGGTTATGGAAGGCGGCCAAGTGGAAATATAAGCCCCCT  
 TTCGGGCATTGCGTACATGTGGTCGTACCATTTAATTGGCCTCATCTGGACTAGTGAATTCA  
 TCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAGTGGTTACTTGTTATTTCAACAGAAGT  
 AAAAATGATCCTCCTGATCATCCCATCCTTTCGTCCTCTCCATTCTCTTCTTACCATCA  
 AGGAACCGTTGTGAAAGGTCATTTTAAATCTCTGTGGTGAGATTCCGAGAATCATTTGTCA  
 TGTACATGCAAAACGCACGTGAAAGAACAGCAGCATGGTGCAATTGTCCAGGTACCTGTTCCGA  
 TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA  
 TACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAATCT  
 TGCCAAGAAGCTCAAGTCATTTACATCTATTAACCTGCTTTGGAGACTTCATAATTTTTCTA  
 GGAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGAGGAGCTCATGGCTTTTAACTACAATCG  
 GGCAATCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTTGCCTACTTAGTAGCCC  
 ATAGTTTTTTATCTGTGTTTGAACCTGTGCTGGATGCACCTTTTCTGTGTTTTGCTGTTGAT  
 CTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT  
 CGTAAAAAGGAGCAACAAATTAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGA  
 ATGAGGAGGGGAACAGAACTCCAGGCCATTGTGAGAT**TAG**ATACCCATTAGGTATCTGTACCT  
 GGAAACATTTCTTCTAAGAGCCATTACAGAATAGAAGATGAGACCCTAGAGAAAAGTT  
 AGTGAATTTTTTTTTTAAAGACCTAATAAACCTATTCTCTCCTCAAAA

**FIGURE 111**

MSGRDTILGLCILALALSLAMMETFRFITTLVHIFISLVILGLLFVCGVLWWLYDYDTNDL  
SIELDTERENMKCVLGFAIVSTGITAVLLVLI FVLRKRIKLTVELFQITNKAISSAPFLLFQ  
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI  
LACQQMTIAGAVVTCYFNRSKNDDPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPIIVM  
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKIL  
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAQVWAVPLLLVAFFAYLVAH  
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN  
EEGTELQAIVR

00990437.111301

**FIGURE 112**

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTCTCTT  
 AGAATAATTTGTATGGGATTTGTGATGCAGGAAAGCCTAAGGGAAAAAGAAATATTCATTCTG  
 TGTGGTGAAAATTTTGTAAAAAAAATTCCTTCTTCAAACAGGGTGCTATTCTGATATT  
**TATG**AGGACTGTTGTTCTCACTATGAAGGCATCTGTTATTGAAATGTTCCCTGTTTGTCTGG  
 TGACTGGAGTACATTCAAACAAGAAAGCCAAAGAAGATTAAAGGCCCAAGTTGCTGAGTGG  
 CCTCAGATCAACTCGGATGTCAAAGCCGGAAAGATCATCGATCCTGAGTTCATTGTGAAATG  
 TCCAGCAGGATGCCAAGACCCCAATACCATGTTTATGGCAGTGACGTGTATGCATCCTACT  
 CCAGTGTGTGTGGCGCTGCCGTACACAGTGGTGTGCTTGATAATTCAAGGAGGAAAAACTT  
 GTTCGGAAGGTTGCTGGACAGTCTGGTTACAAGGGAGTTATTCCAACGGTGTCCAATCGTT  
 ATCCCTACCAGGATGGAGAGAATCCTTTATCGTCTTAGAAAGTAAACCCAAAAAGGGGTGTA  
 CCTACCCATCAGCTCTTACATACCTATCATCGAAAAGTCCAGCTGCCAAGCAGGTGAGACC  
 ACAAAAGCCTATCAGAGGCCACCTATTCCAGGGACAACCTGCACAGCGGGTCACTCTGATGCA  
 GCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCACTTGGCAAGGCCATCCCCCTTCTG  
 CTGCTTTTACCCAGCAGTATCCCCAGACCACAACTCAGTGGGCCACAGGAGCCAGGAGATGGAT  
 CTCCTGGTCCACTGCCACCTACACAAGCAGCCAAACAGGCCAGAGCTGATCCAGGTATCCA  
 AAGGCAAGATCCTTCAGGAGCTGCCTTCCAGAAACCTGTTGGAGCGGATGTCAGCCTGGGGAC  
 TTGTTCCAAAAGGAAGATTGAGCACACAGTCTTTGGAGCCAGTATCCCTGGGAGATCCAAAC  
 TGCAAAATTGACTTGTGCTTTTTAATTGATGGGAGCACCAGCATTTGCCAAACGGCGATTCCG  
 AATCCAGAAGCAGCTCCTGGCTGATGTTGCCAAAGCTCTTGACATTGGCCCTGCCGGTCCAC  
 TGATGGGTGTTGTCAGTATGGAGACAACCTGCTACTCACTTTAACTCTAAGACACACAGC  
 AATTTCTCGAGATCTGAAGCAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTTCTAATGT  
 AGGTCCGGCCATCTCCTTTGTGACCAAGAACTCTTTTCCAAAGCCAAATGAAACAGGAAGCG  
 GGGCTCCAATGTGTTGGTGGTGTGATGGTGGCTGGCCACGGCAAAAGTGGAGGAGGCT  
 TCAAGACTTGGCAGAGACTCAGGAATCAACATTTTCTTATCACCATTGAAGGTGCTGCTGA  
 AAATGAGAAGCAGTATGTGGTGGAGCCCACTTTTGCAACAAGGCCGTGTGCAGAAACAACG  
 GCTTCTACTCGCTCCACGTGCAGAGCTGGTTTGGGCTCCACAAGACCTCGAGCCTCTGGTG  
 AAGCGGGTCTGCGACACTGACCGCTGGCCTGACAGCAAGACCTGCTTGAATCGGCTGACAT  
 TGGCTTCTGTATCGAGGGCTCCAGCAGTGTGGGGACGGGCAACTTCGCGACCGTCTCTCAGT  
 TTGTGACCAACCTCACAAAGAGTTTGAATTTCCGACACGGACAGCGCATCGGGGGCCGTG  
 CAGTACACCTACGAACAGCGGCTGGAGTTTGGGTTTCGACAAGTACAGCAGCAAGCCTGACAT  
 CCTCAACGCCATCAAGAGGGTGGGCTACTGGAGTGGTGGCACCAGCACGGGGGCTGCCATCA  
 ACTTCGCCCTGGAGCAGCTCTTCAAGAACTCCAAGCCCCAACAAGAGGAAGTTAATGATCCTC  
 ATCACCGACGGGAGTCCCTACGACGACGTCCGGATCCAGCCATGGCTGCCATCTGAAGGG  
 AGTGAATACCTATGCGATAGGCGTTGCTCTGGGCTGCCCAAGAGGAGCTAGAAGTCAATGCCA  
 CTCACCCCGCCAGAGCACTCCTTCTTTGTGGACGAGTTTGACAACCTCCATCAGTATGTC  
 CCCAGGATCATCCAGAACATTTGTACAGAGTTTCACTCAGAGCTCGGAAG**TGA**ATTCAAG  
 CAGGCAGAGCACCAAGTGCTGCTTTACTTAACGTGACGTGTTGGACCAACCCACCGCTTAA  
 TGGGGCAGCCAGCGGTGCATCAAGTCTTTGGGCAGGGCATGGAGAAACAAATGTCTTGTATTAT  
 TTCTTTGCGCATGCTGCTTTTTCATATTCCAAAACCTTGGAGTTTCAAAGATGATCACAACGT  
 ATAGAATGAGCCAAAAGGCTACATCATGTTGAGGGTGTCTGGAGATTTTACATTTTGACAAAT  
 GTTTTCAAATAAATGTTCCGAATACAGTGCAGCCCTTACGACAGGCTTACGTAGAGCTTTT  
 GTGAGATTTTTAAGTTGTTATTTCTGATTTGAACTCTGTAACCCCTCAGCAAGTTTTCATTTTT  
 GTCATGACAATGTAGGAATGTCTGAATTAATGTTTAGAAGGATGAAAAATGAAAAA  
 AA  
 AA



**FIGURE 113**

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKC  
PAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSL  
SLPRWRESFIVLESKPKKGVITYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQ  
LLAVTVAVATPTTLPRPSPSAASTTSSIPRPQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQ  
RQDPGAAAFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFR  
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNSRDLKTAIEKITQRGGLSNV  
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE  
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLPVLRVCDTDRLACSKTCLNSADI  
GFVIDGSSSVGTGNFRTVLQFVTNLTKEFEISDTRIGAVQYTYEQRLEFGFDKYSSKPD  
LNAIKRVGYWSGGTSTGAAINFALEQLFKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG  
VITYAIGVAWAAQEELEVIATHPARDHSFFVDEFNHLHQYVPRIIQNICTEFNSQPRN

CAGGATGAAC TGGTTGCAGTGGCTGCTGCTGTGCGGGGGCGCTGAGAGGACACGAGCTCTA  
**TG**CCCTTTCCGGCTGCTCATCCGCTCGGCCCTCTGTGCGCGCTGCTGCCCTCAGCACCATTGGT  
GCGCCAGGTCCCGACGGCTCCGCGCCAGATCCCGCCACTACAGTTTTTCTCTGACTCTAAT  
TGATGCATCGACACCTTGCTGATTTTGGGGAATGTCTCAGAATCCAAAGAGTGTTGAAG  
TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCCTCTGTGTTTGAACAAACATT  
CGAGTGGTAGGAGGACFCCTGTCTGTCTCACTGTCTCTCAAGAAGGCTGGGGTGGGAAGTAGA  
GGCTGGATGGCCCTGTTCCGGGCCCTCTCTGAGAATGGCTGAGGAGGCGGCCGAAAACCTCC  
TCCCAGCCTTTACAGACCCCACTGGCATGCCATATGGAACAGTGAACCTACTTTCATGCGGTG  
AACCAGGAGAGACCCCTGTCACTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC  
CACCTGAGCAGCCTCACTGGTGACCCGGTGTTCTGAAGATGTGGCCAGAGTGGCTTTGATGC  
GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCACATTGATGTGCTCACTGGC  
AAGTGGGTGGCCAGGACGCGAGGCATCGGGCTGCGCTGGACCTCTACTTTGATGACTTTGGT  
GAAAGGAGCCATCTGCTTCAGGATAAAGACTCATGGCCATGTTCTCTAGAGTATACAAAG  
CAATCCGGAAGTACCCGCTTCFAGTAGCTGGTACATGTTGGGTTTCTAGATGTACAAGGGGACT  
GTGTCCATGCCAGTCTTCCAGTCCTTGGAGGCCACTGGCCTGGTCTTCAGAGCCTCATTGG  
AGACATTGACAATGCCATGAGGACCTTCTTCAACTACTACACTGTATGGAAGCAGTTTGGGG  
GGCTCCCGGAATTCTACAACATTTCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA  
CTTCGGCCAGAACTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCACCCCT  
CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTGC GGAT  
TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTCTCTG  
GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCAACTTCATCCACAACATGG  
GTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGGGGCTTGGGGGTACA  
TCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGTGCCAGAGGCTGAAG  
GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGTG  
GAAATTTTCAGAAAAACACTGTTAGTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAAC  
TCTTCTCACCAGAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAACAGAAGGTCCCA  
CTTCTCAGCTGCCCCAGTCAAGCCCTTCACTCCAAAGTTGGCATTACTGGGACAGGTTTCTTCT  
AGACTCCTCAT**TAA**CCACTGGATAATTTTTTATTTTTATTTTTTGGGCTAAACTATAATA  
AATTGCTTTTGGGTATCATATAAA

MPFRLLIPLGLLCALLPQHGHGAPGPDGSAADPAHYSFSLTLIDALDITLLILGNVSEFQRVVE  
VLQDSVDFDIDVNASVFETNIRVVGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKL  
LPAFQTPTGMPYGTVNLLHGVNPGETPVVTTAGIGTFTVEFATLSSTLGDVPFVEDVARVALM  
RLWESRSDIGLVGNHIDVLTGKWAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK  
AIRNYTRFDDWYLVWQMYKGTVSMMPVQSLEAYWPLQSLIGDIDNAMRTFLNYYTVWKQFG  
GLPEFYNI PQGYTVEKREGYPLRPELIESAMYLYRATGDPTLLELGRDAVIESIEKISKVECG  
FATIKDLDRDHKLDNRMESFFLAETVKYLYLLFDPTNFIHNNSGTDFNAVITPYGECILGAGGY  
I FNTAEHPIDLAARLHCQRLKEEQVEDELMREFYSLKRSKSFQKVTSSSGFWEPPARPPT  
LFSPENHDOALRHKPAKQVPLLSCSPQSTSKALLGOVFLDSS

AAAGTTACATTTTCTCTGGAACCTCTCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG  
GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCTGGGCCGGCTCTAGAACA  
ATTACAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT  
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACATGTTCTAGGTCAAACCTGAGTCTACCA  
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT  
ACGCATTGATTCCATGTTTGTCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC  
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCCTGGAGA  
AACAGTGTACTATTCTGTCGAATACCAAGGGGAGTACGAGAGCCTGTACACGAGCCACATCT  
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTGATGTCAGTGTGACATC  
ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCACAGACCTCAGCCTG  
GAGCATCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA  
TCACCAAAGATGGCTTCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTT  
CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG  
GGGTATTCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATATGTGTGAAGCCCCAGA  
CATCTTGTAAGGCCATTGGGAGGTACAGCGCCTTACGCCAGACAGAATGTGTGGAGGTGCAA  
GGAGAGGCCATTCCTCCCTGGTATCTGGCCCTGTTTGCCCTTGTGTGGCTTCATGCTGATCCTTGT  
GGTCGTGCCACTGTTCTGCTGGAATAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGTGG  
TGGTCTCCAGACACCTTGAATAAACAATTACCCAGAAAGTTAATCAGCTGCAGAAGG  
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCCTGGAT  
CTCTAGGTTTGCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACC  
ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA  
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC  
TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGCTGCCACTTGCTGGCTGAGCAACC  
CTGGGAAAAGTGACTTCATCCCTTCGGTCTTAAGTTTTCTCATCTGTAATGGGGGAATTACC  
TACACACCTGCTAAACACACACACACAGAGTCTCTCTCTATATATACACACGTACACATAAA  
TACACCCAGCATTGCAAGGCTAGAGGGAAACTGGTGACACTCTACAGTCTGACTGATTAG  
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT  
GGCTTGGAGAGCCACTTCCAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG  
TGTTGAGTTCACTTCAAGCCCAATGCCGCTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT  
AGGTGACCTGGAGGAAGGTCACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC  
CATGAACTACTGTAAAGTGTTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT  
TGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTCT  
GTGTGGTAAAGTACAGAATTACGCAAATAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA  
AAAAA

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMMWSPVIAIGE  
TVYYSVEYQGEYSESLYTSHIWIPSSWSCSLTEGPECDVTDIDITATVPYNLRVRATLGSQTSAAW  
SILKHFPNRRNSTILTRPNKIEITKDGHRLVIELEDLGPQFEFLVAYWRREPGAEHHVKMVRSG  
GIPVHLETEMPGAAYCVKQKQTFVKAIGFYSAFSQTECEVGEAEPLVLALFAFVGFMILIV  
VVPFLVFMKMRLLQYSCCPVVVLPTLKITINSQKLSICREEVDCALATAVMSPEELLRAWIS

Signal peptide:

amino acids 1-29

## amino acids 230-255

## amino acids 40-43 and 134-137

## amino acids 92-119

## amino acids 232-262

**FIGURE 118**

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCCTT  
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA  
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG  
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT  
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC  
CTGCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA  
GTGATCGCGCCTGGAGAAAACAGTGTACTATTCTGTCTGAATACCAGGGGGAGTACGAGAGCCT  
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGTCTCTGAGTGTG  
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCTAGGGCCACATGGGC  
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTAC  
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG  
GGCCCCAGTTTGAGTTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCCTTGCGGCGCAAGGG  
GTTNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC  
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

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**FIGURE 119**

CGGACGCGTGGGCCGCCACCTCCGGAACAAGCC**ATG**GTGGCGGCGACGGTGGCAGCGGCGTG  
 GCTGCTCCTGTGGGCTGCGGCCCTGCGCGCAGCAGGAGCAGACTTCTACGACTTCAAGGCGG  
 TCAACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG  
 AATGTGGCCAGCGAGTGCGGCTTACAGACCAAGCACTACCGAGCCCTGCAGCAGCTGCACGG  
 AGACCTGGGCCCCCACCACCTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGGCCACAGG  
 AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGCACCTACAGTGTCTCATTTCCCC  
 ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCA  
 GACTTCTGGGAAGGAGCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGG  
 TGGTAGGGGCTTGGGACCCAACCTGTGTGAGTGGAGGAGTGCAGCCCCAGATCACAGCGCTC  
 GTGAGGAAGCTCATCCTACTGAAGCGAGAAGACTT**TAA**CCACCGCGTCTCCTCCTCCACCA  
 CCTCATCCCGCCCACCTGTGTGGGGCTGACCAATGCAAACTCAAATGGTGCTTCAAAGGGAG  
 AGACCCACTGACTCTCCTTCCTTTACTCTTATGCCATTGGTCCCATCATCTTGTGGGGGAA  
 AAATTCTAGTATTTTGATTATTTGAATCTTACAGCAACAAATAGGAACCTCTGGCCAATGAG  
 AGCTCTTGACCAAGTGAATCACCAGCCGATACGAACGCTCTGCCAACAAAAATGTGTGGCAAA  
 TAGAAGTATATCAAGCAATAATCTCCCACCCAAGGCTTCTGTAAACTGGGACCAATGATTAC  
 CTATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC  
 CAAATAGGAGGCATTCAATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTATCAAT  
 AAAAACTTGCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT  
 GTTATTTCTCTGTATTATTTTCTTATTACAAAAGAAATGCAAGTTCATTGTAACAATCCA  
 AACAATACCTCACGATATAAAAAATAAAATGAAAGTATCCTCCTCAAAA

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**FIGURE 120**

MVAATVAAAWLLWAAACAQQEQDFYDFKAVNIRGKLVSLVKYRGSVSLVVNVASECGFTDQ  
HYRALQQLQRDLGPHHFNVLAFCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG  
AHPAFKYLAQTSKGKEPTWNFWKYLVPDQKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

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**FIGURE 121**

CGGACGCGTGGGCGGGCCGGGACGCAGGGCAAGCGAGCCTATGGCTGTCTACGTGGGATGC  
 TCGCCTTGGGGAGGCTGTGCGCGGGAGCTCGGGGGTGTCTGGGGCCCGGGCCGCTCTCT  
 CGGAGTTGGCAGGAAGCCAGGTTGCGAGGGTGTCCGCTTCCTCAGTTCAGAGAGGTGGATCG  
 CATGGTCTCCACGCCCATCGGAGGCCCTCAGCTACGTTTACGGGTGCACCAAAAGCATCTTA  
 ACAGCAAGACTGTGGGCCAGTGCCTGGAGACCACAGCACAGAGGGTCCCAGAACGAGAGGCC  
 TTGGTCGTCTCCATGAAGACGTTCAGGTTGACCTTTGCCCAACTCAAGGAGGAGGTGGACAA  
 AGCTGCTTCTGGCCTCCTGAGCATTGGCCTCTGCAAAGGTGACCGGCTGGGCATGTGGGGAC  
 CTAACCTCTATGCATGGGTGCTCATGCAGTTGGCCACCGCCAGCGGGCATCATTTCTGGTG  
 TCTGTGAACCCAGCCTACCAGGCTATGGAAGTGGAGTATGTCTCAAGAAGGTGGGCTGCAA  
 GGCCCTTGTGTTCCCCAAGCAATTCAGACCCAGCAACTACAACTCCTGAGCAGATCT  
 GTCCAGAAGTGGAGAATGCCAGCCAGGGGCCCTTGAAGAGTCAGAGGCTCCCAGATCTGACC  
 ACAGTCATCTCGGTGGATGCCCTTTGCGGGGACCTGTCTCTGGATGAAGTGGTGGCGGC  
 TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATCAACCAGCAGTTCTCTGTCTGCCATG  
 ACCCATCAACATCCAGTTCACCTCGGGGACAACAGGCAGCCCCAAGGGGGCCACCTCTCC  
 CACTACAACATTGTCAACAACCTCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGAC  
 ACCAGAGCAGTTGCGGATGATCTGCCCAACCCCTGTACCATTGCCTGGGTTCGCTGGCAG  
 GCACAATGATGTGTCTGATGTACGGTGCCACCTCATCTGGCCTTCCCATCTTCAATGGC  
 AAGAAGGCATCGGAGGCCATCAGCAGAGAGAGAGGCCACCTTCTGTATGGTACCCCCACGAT  
 GTTCGTGGACATTCTGAACACAGCCAGCACTTCTCCAGTTATGACATCTCGACCATGTGTGGAG  
 GTGTCAATTGCTGGGTCCCTGCCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAT  
 ATGAAGGACCTGGTGGTTGCTTATGGAACACAGAGAACAGTCCCCTGACATTCCGCGCACTT  
 CCCGTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAAATTATGGCTCACACGGAGG  
 CCCGGATCATGAACATGGAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGC  
 ATCCGAGGGTACTGCGTCATGCTGGGCTACTGGGTGAGCCTCAGAAGACAGAGGAAGCAGT  
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTGCCACAATGAATGAGCAGGGCTTCTGCA  
 AGATCGTGGGGCGCTCTAAGGATATGATCATCCGGGGTGGTGAAGACATCTACCCCGCAGAG  
 CTCGAGGACTTCTTTACACACACCCGAAGGTGCAGGAAGTCAGAGTGGTGGGAGTGAAGGA  
 CGATCGGATGGGGGAAGAGATTGTGCCTGCATTCCGGCTGAAGGACGGGAGGAGACACGG  
 TGAGGAGATAAAAGCTTTCTGCAAAGGGAAGATCTCTCAGTTCAAGATTCCGAAGTACATC  
 GTGTTTGTCACAAACTACCCCTCACCATTTTCAGGAAAGATCCAGAAATTCAAACTTCGAGA  
 GCAGATGGAACGCACATCTAAATCTGTGAATAAAGCAGCAGGCTGTCTGGCCGGTGGCTT  
 GACTCTCTCCTGTCAAGATGCAACCTGGCTTATGCACCTAGATGTCCCAGCAGCCAGGTTT  
 TGAGCCAGGCACATCAAAATGTCAAGGAATTGACTGAACGAAGTCAAGAGCTCTGGATGGGTC  
 CGGGAACCTCGCCTGGGCGACAGGTGCCAAAAGGCAGGCAGCCTGCCAGGCCCTCCCTCCTG  
 TCCATCCCCACATTCCTCTGTCTGTCTTGTGATTGGCATAAAGAGCTTCTGTTTTCTTT  
 GAAAAAAAAAAAAAAAAA

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**FIGURE 122**

MAVYVGMRLRLGRLCAGSSGVLGARAALSRSWQEARLQGVRFLSSREVD RMVSTPIGGLSYVQ  
 GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG  
 DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY  
 YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLPGTLLLDDEVVAAGSTRQHLDQLQYN  
 QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY  
 HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFlyGTPTMFVDILNQPDFSSY  
 DISTMCGGVIAGSPAPPELIRAIINKINMKDLVAYGTTENSPVTFahfPEDTVEQKAESVG  
 RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPOKTEEAVDQDKWYWTGDTVAT  
 MNEQGFCIKVGRSKDMIIRGGENIYPAELEDDFFHHPKVQEVQVVGVKDDRMGEEICACIRL  
 KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

**Signal Peptide:**

amino acids 1-22

**Transmembrane Domains:**

amino acids 140-161, 213-229, 312-334

**Putative AMP-binding Domain Signature:**

amino acids 260-271

**N-myristoylation Sites:**

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,  
 314-319, 318-323, 379-384, 380-385, 409-413

**N-glycosylation Site:**

amino acids 282-285

**FIGURE 123**

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA  
TGATCCTGCCCAACCCCTGTACCATTGCCTGGGTTC CGTGGCAGGCACAATGATGTGTCTG  
ATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACTGGAGGC  
CATCAGCAGAGAGAGAGGCACCTTCTGTATGGTACCCCCACGATGTTTCGTGGACATTCTGA  
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC  
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT  
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTTCCCTGAGGACACTGTGG  
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG  
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT  
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT  
ATTGGACAGGAGATGTCGCCAC

0090437.1.1601

**FIGURE 124**

GAGCAGGACGGAGCC**ATG**GACCCCGCAGGAAAGCAGGTGCCAGGCCATGATCTGGACTGC  
 AGGCTGGCTGCTGCTGCTGCTTCCGCGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG  
 TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGC GCGCCGGGC  
 GTGGACGTCTGCACCGAGGCCGTGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC  
 AGTGCGGGGTTCGCGTTTCGGGACTCCCCGGCAAGAATGACCGCGCCTGGATCTTCACGGGC  
 TTCTGGCGTTTCATCCAGCTGCAGCAATGCCTCAGGATCGCTGCAACGCCAAGCTCAACCTC  
 ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCCGCCAACGGCGTGGAGTG  
 CTACAGCTGTGTGGGCCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCGGTCTGTAGCT  
 GCTACAACGCCAGCGATCATGTCTACAAGGGTGCTTCGACGGCAACGTACCTTGACGGCA  
 GCTAATGTGACTGTGTCTTGCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACCTCGGGA  
 TGGAGTAACAGGCCCAGGGTTCACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAAT  
 CTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATCCCACCCCTTGTCGGGTGCCCCCT  
 CCAGAGCCCACGACTGTGGCCTCAACCACATCTGTCAACACTTCTACCTCGGCCCCAGTGAG  
 ACCACATCCACCACCAACCATGCCAGCGCCAACCACTCAGACTCCGAGACAGGGAGTAG  
 AACACGAGGCCTCCCGGGATGAGGAGCCAGGTTGACTGGAGGCGCCGTGGCCACCAGGAC  
 CGCAGCAATTCAGGGCAGTATCTGCAAAAGGGGGCCCCAGCAGCCCCATAATAAGGCTG  
 TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTG**T**  
**GA**GCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT  
 CATCACTTCTGTTCACCACCTGGACTGGGCTGGCCAGCCCTGTTTTCCAACTTCCC  
 CAGTATCCCCAGCTTCTGCTGCGCTGGTTTGCGGCTTTGGGAAATAAAATACCGTTGTATAT  
 ATTCTGCCAGGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTGTCTC  
 TCCGCTTGCTCTTGTGTATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACGGGGAAGGTG  
 AGAGAGAGGATGCTAAGCTTCTACTCACTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGG  
 GGTGGGTGGGACAATGGCTCCCCACTCTAAGCACTGCCTCCCTACTCCCGCATCTTTGGG  
 GAATCGGTTCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCGGTAC  
 CCAATTCGCCCTATAGTGAGTCGTA

**FIGURE 125**

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSVCVKADDGCSFNKMKTVKCAPGVDVCT  
EAVGAVETIHGQFSLAVRGCSSGLPGKNDRGLDLHGLLAFIQLQQCAQDRCNAKLNLSRAL  
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGCDFGNVTLTAANVTV  
SLPVRGCVQDEFCTRDGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRIPLVRLPPPEPTT  
VASTTSVTTSTSAFVRPTSTTKMPAPTSQTPRQGEHEASRDEEPRLTGGAAGHQDRSNSG  
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSVCVKADDGCSFNKMKTVKCAPGVDVCT

CGGGACTCGGCGGGTCTCTCTGGGAGTCTCGGAGGGGACCGGCTGTGCAGACGCC**ATG**GAGT  
TGGTGTCTGGTCTTCTCTGCAGCCTGTCTGGCCCCATGGTCTTGGCCAGTGCAGCTGAAAAG  
GAGAAGGAAAATGGACCCCTTTTCATTATGATTACCAGACCCCTGAGGATTGGGGGACTGGTGTT  
CGCTGTGGTCTCTCTCGGTTGGGATCCTCCTTATCCTAAGTCGCAGGTGCAAGTGCAGTT  
TCAATCAGAAGCCCCGGGCCCCAGGAGATGAGGAAGCCCCAGGTGGAGAACCTCATCACGCC  
AATGCAACAGAGCCCCAGAAGCAGAGAAC**TGA**GTGCAGCCATCAGGTGGAAGCCTCTGGAA  
CCTGAGGCGGCTGCTTGAACCTTTGGATGCAAA**TG**TCGATGCT**TAA**GAAAACCGGCCACTTC  
AGCAACAGCCCTTCCCCAGGAGAAGCCAAGAACTTGTGTGTCCCCACCCATATCCCCCTTA  
ACACCATTCTCCACCTGATGATGCAACTAACACTTGCCCTCCCCACTGCAGCCTGCGGTCTT  
GCCACCTCCCGTGATGTGTGTGTGTGTGTGTGTGACTGTGTGTGTTTGCTAACTGTG  
GTCTTTTGGGCTACTTGTTTGTGGATGGTATTGTGTTTGTAGTGAATCTGGACTGCGCTT  
CCCAGGCAGGGGCTGAGCCACATGGCCATCTGCTCCTCCCTGCCCGTGCCCTTCCATCAC  
CTTCTGCTCTAGGAGCGCTGTTGTGTGCCGAGACCCGCCCCCTCCCTGATTAGGAGATGC  
TAGGGTAAAGAGCACGGGCGAGTGGTCTTCAGTCTGTCTGGGACTGGGAAGGTTTGCAGCAC  
TTTGTGCATATTCTTCATGGACTCCTTTCACCTCTTTAA**CA**AAAACTTGCTTCTTATCCC  
ACCTGATCCAGCTCTGAAGGTCTCTTAGCAACTGGAGATACAAAGCAAGGAGCTGGTGAAGC  
CAGCGTTGACGTGAGGCAGGCTATGCCCTTCCGTGGTTAATTTCTTCCAGGGGCTTCCAGC  
AGGAGTCCCACATGCCCCGCCCCCTTACAGAGCGCCCCGGGATTCCAGGCCAGGGCTTCT  
ACTCTGCCCCTGGGAATGTGTCCCTGCATATCTTCTCAGCAATAACTCCATGGGCTCTGG  
GACCTACCCCTTCCAACCTTCCCTGCTTCTGAGACTTCAATCTACAGCCAGCTCATCCAG  
ATGCAGACTACAGTCCCTGCAATTGGGTCTCTGGCAGGCAATAGTTGAAGGACTCCTGTTCC  
GTTGGGGCCAGCACACCGGGATGGATGGAGGGAGAGCAGAGGCCTTTGCTTCTTGCTTACG  
TCCCCTTAGATGGGCAGCAGAGGCAACTCCCGCATCCTTTGCTCTGCCTGTCCGTGGTCAG  
GCGGTGAGCGAGGTGGGTTGGAGACTCAGCAGGCTCCGTGCAGCCCTTGGGAACAGTGAGAG  
GTTGAAGGTCATAACGAGAGTGGGA**ACTCA**ACCAGCATCCCGCCCTCCTGTCTCTGTGTTAT  
CCCCGGAAACCAACCA**AA**ACCTGCGCTGTGAGC**CA**TTCCGCTTCTCTGTA**CT**CGTGA**CT**AT  
CCTCAACAACAACAGAAAAAGGAATAAATATCCTTTGTTTCTT

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**FIGURE 127**

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK  
CSFNQKPRAPGDEEAQVENLITANATEPQKQRTREVQPSGGSLWNLRRLLEPLDANVDA

00000427-111601

**FIGURE 128**

AAACTTGACGCCATGAAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT  
CCTCTCTGCCAGGGAGCCACCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG  
CGTCACGACCCGAGGCCTTTAAACACCCCGTTCCCTGAACATCGACAAATTGCGATCTGCGTTT  
AAGGCTGATGAGTTCTGAAGTGGCAGCCCTCTTTGAGTCTATCAAAAGGAAACTTCCTTT  
CCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAGT  
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT  
CTTTCCTGCCTCAGGAAGTCCAATAAAACATTTCCATCCAAA

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**FIGURE 129**

MKIPVLPVVLSSLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSAFKADE  
FLNWHALFESIKRKL PFLNWD A FPKLKGLRSATPDAQ

109111.2510000

**FIGURE 130**

CAGTTCGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC  
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCCAGGTGTTTC  
TTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC  
TTTGCCGGCCACTCTGAGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCT  
TCATGATTTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCTCA  
AATTTTTGTTATACTAGATGGCTTCCATTTACCCACCCTATTTTAAGGTCCCTTTATTTTT  
AGGTTCAAGGTTTCACTTGAGAAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTTTATC  
TTCATATTAATTGTAACGATTAATAAAGAATAAGAGCAGCAGACCTCTAGGAGAATATTT  
TATCCCTGGGTGCCCTGACACATTTATGTAGTGATCCACAAATGTGATTGTTAATTTAA  
TGTTATTCTAATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT  
AAAAGTTTGTAGTATATTTTTCACTAGATATTTGTATAGAAAGACTGAATAGTGATG

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**FIGURE 131**

MGVEIAFASVILTCLSLAAGVSQVVLLQFPVPTQETGPKAMGDLSCGFAGHS

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103777 1640660

**FIGURE 132**

GGGGAATCTGCAGTAGGTCTGCCGCGCATGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG  
 GCTGCTGTTGTTCTCTCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGA  
 AAGTATTTATTGACCAAAATTAACAGGTCCTTGGAGAATTACGAACCATGTTCAAGTCAAAC  
 TGCAGCTGCTACCATGGTGTCATAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG  
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA  
 GACTGTACCGGGAAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT  
 TTGGAAGTATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA  
 GGTTCCTAAATGGATGGAGCCTGCCATCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC  
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGACCTGCTGTTTGGCCAATTTAT  
 CCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGCAGCACAGTG  
 GCCATGGA AAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG  
 ATCCTCTCATCTCTGTCTCGGAAAAACCCAAAACCTTGTTGATGCAGAAATACACCAAAAAC  
 CAGGCCTGGAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT  
 GGATCACTGCAAAATACAAGTATCTGTTTAAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA  
 AACACCTCTTCTGTGTGGCTCACTGTTTTCCATGTTGGTGATGAGTGGCTAGAATTCTTC  
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAAACAGATCTCTCCAATGTCCA  
 AGAGCTGTTACAATTTGTAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA  
 GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG  
 AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTTAT  
 TCCCAAAATGTTGAAAATGAACATATAGTAGTCATCATAGGACCATAGTCCTCTTTGTGGCA  
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA  
 TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA  
 AAGATTTAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTGGATGAATAAGGA  
 CCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTCATTTTCTTAAGACCAATC  
 ACAGCTTGTGCCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATGACTGTGTCCA  
 TGTGATGATGCCCTTTGTCCATTATTTGGAGCAGAAAATTCGTCAATTTGGAAGTAGTACAA  
 CTCAATTGCTGGAATTGTGAAATTAATCAAGGCGTGATCTCTGTCACTTTATTTTAATGTAGG  
 AAACCCATAGGGGTTTATGAAAAATACTTGGGGATCATCTCTGAATGGTCTAAGGAAGCGG  
 TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTTGTAAAACCATAAACTCTGTACTCAG  
 GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATT  
 TCAGGTTCCCTTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAA

**FIGURE 133**

MEWWASSPLRLWLLFLLLPSAQGRQKESGSKWKVFIDQINRSLENYEPSSQNCSCYHGVIE  
EDLTPFRGGISRKMMAEVVRRKLGTHYQITKNRLYRENDCMFPSRCSGVEHFILEVIGRLPD  
MEMVINVRDYPQVPKWMEPAIPVFSFSKTSEYHDIMYPAWTFWEGGPAVWPIYPTGLGRWDL  
FREDLVRSAAQWPWKKKNSTAYFRGSRTSPERDPLILLSRKNPKLVDAEYTKNQAWKSMKDT  
LGKPAAKDVHLVDHCKYKYLENFRGVAASFRFKHLFLCGSLVFHVGDWLEFFYPQLKPWVH  
YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMDDITCYWENLLSEYSKFLSY  
NVTRRKGYDQIIPKMLKTEL

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CACCCCTCCATTCTCGCC**ATG**GCCCTGCACCTGCTCCTGATCCCTGCTGCCCTGCCTCTT  
TCATCCTGGCCCTTTGGCACCGGAGTGAGATTCTGTGCGCTTTACCTCCCTTCGCCCACTTCTT  
GGAGGGATCCCGGAGTCTGGTGGTCCGGATGCCCGCCAGGGATGGCTGGCTGCCCTGCAGGA  
CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTGTGTGGGCAGC  
ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCTTCAG  
AGGTCACTGTATGTGGCTGCACTGCCCTGGCCTGCAGCTGGTGATGCGGTACTGGAGCC  
CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCGC  
TCCTCTGCTTTGTGCTCCATGTCATCTCCTGGCTCCTCATCTTAGATCCTTCTCGTCTT  
GACTATGCTGAGCTCATGGGCCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCAGCC  
TCTGGCCCTGAACTCTCCCGGGCTCTCAGACTCTTCTCCCACTGCGCCACCCAGTGTGTG  
TGGAGCTGCTGACAGTGCTGTGGGTGGTGCCACCTGGGCACGGACCGTCTCCTCCTTGCT  
TTCCTCCTTACCCTCTACCTGGGCCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT  
CCGGGCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGGGCCCAGGATGGGGAGGCAGAG**T**  
**G**AGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCTCTCCCACTGAATTCTAAATCCTTAAC  
ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAATCCATGGACTGAAGGAGATGCCCTT  
CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCTTAAATCTGAGTTTCAGCCA  
CTGAACCTCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC  
TTCACTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGATCATGCC  
CTGACCACTCCCCTGGCAGCTGTTACTTGCCTCTGCGCCTCAGGGTCCCCCTTGTGACCCGT  
GGCTTCCACTCCAAGAAGGTGGACACGGGCTCGAAGTTCAACGGTCATAGCTGTCCCTCCA  
GGCCCAACCTTGACCTCACACTCCCGGCCCTAGTCTCTGACCTCCTTAGGCCCTGCCTCT  
GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAACTCGATGACTTGGGGCTC  
CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAAATAAAGTCAGCCTTTTTCTAAAAAAA

**FIGURE 135**

MAPALLLI PAALASFI LAFGTGV EFRVFTSLRPLLGGI PESGGF DARQGWLAALQDRSILAP  
LAWDLGLLLL FVQGHS LMAAERVKAWT SRYF GVLQRSIYVACTALAIQLVMRYWEP I PKGPV  
LWEARAEPWATWV PLLCFVLHV ISWLLI FSI LLVFDYAEIMGLKQVYYHVLGLGEPLALKSP  
RALRL FSHLRHPVCVELLTVLWVVP TLTGDRLLLAFLTLTYLGLAHLSDQDQLRYLRAQLQR  
KLHLLSRPQGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

**FIGURE 136**

CCGAGCACAGGAGATTGCGCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA  
 AGAAATTGCCAAACCATGTCTTTTTTCTGTTTTTCAGAGTAGTTCACAACAGATCTGAGTGT  
 TTTAATTAAAGCATGGAATACAGAAAACAACAAAAAAGCTTAAGCTTTAATTTTCTGGAATT  
 CCACAGTTTTCTTAGCTCCCTGGACCCGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA  
 TCACGTGGTGTCTCCGACTACTCACCCGAGTGTAAGAACCCTTCGGCTCGCGTGCTTCTG  
 AGCTGCTGTGGATGCGCTCTCTGGACTGTCCTTCAGAGTAGGATGTCACTGAGATCC  
 CTCAATGGAGCCTCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT  
 TCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTT  
 ACAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAAATCCATTT  
 CTGGTCACTTCTGGTGACCTCCCACCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC  
 TTGGGGTGAAAAAAGTCTTGGTGGGATATGAGGTTCTTACATTTTCTTATTAGGCCAAG  
 AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCCTTAGAGGATGAACACCTTCTTTATGGT  
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATATTAGGC  
 ATTCAGGTGGTAACTGAGTTTTTGCCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG  
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTAAACCTAAACCACTCAGAGAAGTTT  
 TTCACAGGTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAACCCATAT  
 TTCTTACCAGGATATCCTTTCAAGGTGTTCCCTCCATCTGCAGTGGGTGGGTTATATAA  
 TGTCAGAGATTTGGTGCCAAGGATCTATGAAATGTGGGTACGTAATAAACCCCATCAAGTTT  
 GAAGATGTTTATGTGCGGATCTGTTGAATTTTATAAAGTGAACATTATATTCAGAAGA  
 CACAAATCTTTTCTTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG  
 CAGCCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTTTGGCAGGTATGCTAAGGAACACC  
 ACATGCCATTATTAACCTTCACATTCTACAAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA  
 GTGTTAAATAAAGTAGGTACTGTGGAATAATCATGGGAGGTGAGTGTGCTGGCTTACACTG  
 AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGTTTACACTGTGATTATTAGTCT  
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTTGTCTAAA  
 GAAATTAATAGGACCAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAGGG  
 TGTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAAACAATGTAGAGTTTTATTATTG  
 AACAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGATTACCAATTTAAAAATATA  
 TGTAGTCTGTGTCAAAAACCTTCTTCACTGAAGTTATACGAACAAAATTTTACCTGTTTT  
 TGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTAAAAATTA  
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAAT  
 CATTCTTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC  
 TCCATTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTGGACTTGTGTTAAAT  
 ATTTTACTGTGGTAATATAGAGAAGAATTAAAGCAAGAAAACTCTGAAA

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**FIGURE 137**

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQD  
FHFTLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EK  
EDKMLALSLEDEHLLYGDIIRQDFLDTYNNLTTLKTIMAFRWVTEFCPNAKYVMKTDTDVFIN  
TGNLVKYLNLNLHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPFYCSGLGYIMSRD  
LVPRIYEMMGHVKPIKFEDVYVGICLNLLKVNIIHIPEDTNLFFLYRIHLDVCQLRRVIAAHG  
FSSKEIITFWQVMLRNTTCHY

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**FIGURE 138**

CCTCTGTCCACTGCTTTTCGTGAAGACAAGATGAAGTTTACAATTGTCTTTGCTGGACTTCTT  
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA  
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACAATGTGGCCAATGTTGACA  
ATAACAACGGATGGGACTCCTGGAATTCCATCTGGGATTATGGAATGGCTTTGCTGCAACC  
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAAATGAACAAGGAAGTCATGCCCTCCAT  
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC  
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA  
AAAAACATTGCAAACATGTGTCGTGGGATTCCAACATACATGGCTGAGGAGATGAAGAGGC  
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGACTATGGATTGTGGACATTT  
CCTTCTGTGGAGACACGGTGGAGAACTTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT  
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCAATCTGAAATT  
TTTCTCTACTAGTTATGTTTGATTCTTTAAGTTTCAATAAAATCATTAGCATTGAAAAAAA

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**FIGURE 139**

MKFTIVFAGLLGVFLAPALANYNINVNDDNNNAGSGQQSVSVNNEHNVANVDNNGWDSWNS  
IWDYGNNGFAATRLFQKKTCIVHKMNKEVMPSIQSLDALVKEKKLQKGPGGPPPKGLMYSVN  
PNKVDDLKFKGNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

**Signal Peptide:**

amino acids 1-20

**N-myristoylation Sites:**

amino acids 67-72, 118-123, 163-168

**Flavodoxin protein homology:**

amino acids 156-174

05990437.11504

**FIGURE 140**

CATTTCTGAAACTAATCGTGTGACAGAAATTGACTTTGAAAAGCATTGCTTTTACAGAAGTATA  
 TTAACCTTTTAGGAGTAATTTCTAGTTTGATTGTAATATGAAATAATTTAAAGGGCTTCG  
 CTCATATATAGGAAAATCGCATATGGTCCTAGTATTAAATCTTATTGCTTACTGATTTTTT  
 TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAA  
 GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGCTGGTTTGTTTACATG  
 CAAGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGT  
 TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT  
 CAGATTCCGTTGCCAACTCGTCCCCATTGGTTTCTTCTTTTGGTACTACAGAAGAGGAAAT  
 CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTAC  
 TGGAAAAGAAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCAAATTTAAAGCAAAGGGA  
 TTGAATCCGGATGGAACCTCAGCCCTTCAACCTGGGTGGATTTTCTCCAGCCTCCAAGCC  
 ATCATCACCAGAGAAGTAAAAGCTGAAGAGAAATCACCATCTCCATTAATGTGAAGACAG  
 TCAAAAAGAACCTGAGGATAGACAACAGGCTTCAAAAAGCCCTTACAATGGTGTAAGAAAA  
 GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCAG  
 TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGCGGAGTCGATCTGGAACATACA  
 GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAGGCCCTCGAAGACATCATAATCAT  
 GGTTCTCCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGACATGG  
 TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG  
 CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT  
 GAGAGGTCCCATAAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG  
 CTGAATTTCTCTTCTTTGAGCCTGCATCAGTTCTTGGTTTTTGCCTATCTACAGTGTGATGT  
 ATGGACTCAATCAAAAACATTAAACGCAAACTGATTAGGATTTGATTTCTTGAACCCCTCTA  
 GGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAGAAGTATGTTAATTTTTTGCACATT  
 AAAATGCCCTAGCAGTATCTAATAAAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT  
 TGTGTATTGTTTATTGCTATAAGAACTGGAGCGTGAATTCTGTAAAAATGTATCTTATTTTT  
 ATACAGATAAAATTGCAGACACTGTTCTATTAAAGTGGTTATTTGTTTAAATGATGGTGAAT  
 ACTTTCTTAACACTGGTTTGTCTGCATGTGTAAGATTTTTTACAAGGAAATAAAATACAAAT  
 CTGTTTTTTTCTAAAAAAGGAGT

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 109117 140660

**FIGURE 141**

MNDSLRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLFLFGTTEEEIQEICIETLRLY  
TRKKPNYELLEKEVEKRVKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK  
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSRTSRSRSHTPRRHYN  
NRRSRSGTYSSRSRSRSHSESPPRRHHNHGSPHLKAKHTRDDLKSSNRHGHRKKRSRSRQ  
SKSRDHSDAKKHRHERGHRDRRERSRSFERSHKS KHHGGSRSRGHRHR

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**FIGURE 142**

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA  
TTTTTTGAANNATTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTACAGAAATATAT  
TANCTTTTTAGAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAAGGGCTTCGCT  
CATATATAGGAAAAATCGCATATGGTCCTAGTATTAAATTNTTATTGCTTACTGATTTTTTTTG  
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA  
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATGCA  
AGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT  
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA  
GATTCGGTTGCCAACTNGTCCCATTTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAATCC  
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTACTG  
GAAAAAGAAGTAGAAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTAAGCAAGGGATT  
GAATCCGGATGGAATCCAGCCCTTTCAACCCCTGGGTGGATTTCCTCC

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**FIGURE 143**

GGACACGAGGCTCGTGCCAAAGCTTGGCACGAGGGTGACCGCTTCTCGCACGCGTCA**ATG**GC  
 GGTCCTCGGAGTACAGCTGGTGGTGACCTGCTCACTGCCACCCTCATGCACAGGCTGGCGC  
 CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTTTGTTCGATACAAGCACCCG  
 TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG  
 GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCGAGATGCCCCGTTCCAGCTGG  
 AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGCTTCTTCTGGAGTACCACTGG  
 TTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTTACAGAGGCCTACTACTACAT  
 GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCACGGTGACCTTCT  
 CCATCAAGATGTTCTTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGTGAGCGC  
 TCTGTCTGCCTCACCTTTGCCCTTCTTCTGCTGCTGGCCATGCTGGTGCAAGTGGTGGC  
 GGAGGAGACCTCGAGCTGGGCTGGAGCCTGGTCTGGCCAGCATGACCCAGAAGCTTAGAGC  
 CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCTGTGGCCAAAGCTGGCTATCCGCGTG  
 GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCTCACCTTCCCAGGCCGCGGCTGGC  
 CCAGACCCACCGGGACGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCTCCTGTC  
 ACACAGCTTCTGTCTCCCCTGTTTCATCCTGTGGCTCTGGACAAAGCCATTGCACGGGAC  
 TTCCTGCACAGCCGCGCTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCCTCGA  
 CTCTGGGCGCCTCTGCTTGTGCTGGTGGTGTGCTGTGCTGCTGCGGCTGGCGGTGACCCGGCCCC  
 ACCTGCAGGCCCTACCTGTGCTGGCCAAAGGCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC  
 CGCATCGAAGCCCTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT  
 GAGCTTGCACTACCTGACGCCGCTCATCCTCACCTCAACTGCACACTTCTGCTCAAGACGC  
 TGGGAGGCTATTCTGGGGCCTGGGCCCAGCTCCTTACTATCCCCGACCCATCCTCAGCC  
 AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG  
 GGCCCTGGGTGGCTGCTTACTCCCCTTCTCCTCGTGGCGTCTTGGCCTACCTCATCTGGT  
 GGACGGCTGCCTGCCAGCTGCTCGCCAGCCTTTTCGGCCTTACTTCCACCAGCACTTGGCA  
 GGCTCC**TAG**CTGCCTGCAGACCTTCTGGGGCCCTGAGGTCTGTTCTTGGGGCAGCGGGACA  
 CTAGCCTGCCCCCTCTGTTTGGCGCCCCGTGTCCCAGCTGCAAGGTGGGGCCGGACTCCCC  
 GCGGTTCCCTTCCACACAGTGCCTGACCCGCGGCCCCCTTGGACGCCGAGTTTCTGCCTCA  
 GAACTGTCTCTCCTGGGCCAGCAGCATGAGGGTCCCAGGCCATTGTCTCCGAAGCGTATG  
 TGCCAGGTTTGAGTGGCGAGGGTGATGCTGGCTGCTCTTCTGAACAAATAAAGGAGCATGCC  
 GATTTTTTAA

**FIGURE 144**

MAVLGVQLVVTLLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE  
RWANGLSEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY  
YMLGPAKETNIAVFWCLLTVTFSIKMFLT VTRLYFSAEEGERSVCLTFAFLFLLLAMLVQV  
VREETLELGLEPGLASMTQNLEPLLKKQGDWALPVAKLAIRVGLAVVGSVLGAFLTFPGLR  
LAQTHRDALTMSEDRPMLQFLHLSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA  
FDSGRLWLLVVLCLLR LAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVVRVYCYVT  
VVS LQYLTPLILTINCTLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVVQQTAAARI  
AGALGGLTPLFLRGVLAYLIWWTAACQLLASLFGLYFHQHLGS

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CGTTNGCACGCGTCAATGGCGGTCCTCGGAGTACAGCTGGTGGTGACCCTGCTACTGCCAC  
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTT  
TGTTCCGATACAAGCACCCGNTTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC  
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC  
GAGATGCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGC  
TTCTTCTGGAGTACCACTGGTTTGTGGACTTTGCTGTGTACTCGGGCGCGGTGTACCTCTT  
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT  
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTCTGACAGTGACACGGCTGTACTTACG  
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTTGCCTTCTCTTCTCTGCTGCTGGC  
CATGTCTGGTGCAAGCG

GGTTCTACATCCTCTCACTGAGAATCAGAGAGCATATCTTCTTACGGCCCGCTGATTATTAAAGCTGGCTT  
AATCTGAAGGTTTCTCACTCAAAATCTTTTGATGATCTGATTGTGGGGGACATGGCAAGCTTTGTCTTAAAGACGC  
TTGGCTGGTTTGGGCCGTTTGACTGACAGAAAGTGGCCAGGGAGAATTCAGCACACTGCTCGGAGAATGAAGG  
CGCTTCTTGCTGGTCTTGCTTGGCTCAGCTGCTCTTAACATCATTGACATCTGGGCAACTGCATCTCTGT  
TATTCAAGATCTTAAAGGTGCTTCCCATACGCCGTACCAAAAGATAGGAAGAGCGCTCACAAGATGGCTG  
TCAGACGGCTGTGCGAGCTCAGACGACGGCTCTCCCTCCGAGAGTTTCTGCAGCTGCCACCATCTCTTT  
TGACAGCAGGCTTGGCTAGACAACCTGCTACGTGTTCTCGGAGAGCGGGACGAGCAATCAGGCCCA  
GTGGACTCTGGCCGGAGCAGCAAGCAATAGGCCAGCGCCCTTTGAGAGATCACTATTGAAGCAGATCAATTTAA  
AAAAATAAATCAAGCTTTGAGTTGTTCTTCAGAGACAAGAGCGGGATGCAGTTGCCAACCTGCGCAGCAAGG  
GACGAGAAAATTTGAAACAACCATGCCCTGAAGTCTTTCCAAAGTTTGACCACTGATTCATAGATGGTGAA  
ATTACAGCACTCAAGATCAATCGAGTAGATCCAGTGAAGCGCTCTATTAGCTGTGGTGGAGTAGCAAAAC  
CCCACTGGTCCATATTCAATTAACAACAATTTATCTGTATGGGTGATGCGCGAGAGCGCCGCGTACTCGCG  
GACACATCATTTCAAAGTCAACGGGATGGACATCAGCAATTCCTTCAACAATACGCTGTGGCTGTCTCTGGG  
CAGCCCTCCGAGGTGCTGTGGCTGATGTGATGGTGAAGAACAATTCGCGACAGGAACAATGGACAGCGCCC  
GGATGCTCAACGACCCGAGATGACAGCTTTCTATGTTCTCAACAAAATAGCCGCCGAGAGACGCTTGGAA  
TAAACTGGTGGCGCAAGGCTGGATGAGCTGGGGTTTTCATCTCAATGTGCTGGATGGCGGTGTGGCATATCGA  
CATGTGTCGTTTGGAGGAATGACGGTCTTTAGCATCAATGAGGATGATTCGATATGGCAGCCGAAAG  
CGCGCTCATCTTGTCAAGCATGTGATGAAGACGTGTTCACTGCTGTGTGTCGCGGACGCTCGCGACGGAGCC  
CTGACATCTTTGAGGAAGCCGGCTGGAACGCAATGGACGCTGGTCTCCGAGGCGAGGGAGAGGACCAACT  
CCCAAGCCCTCCATCTCAATTACTTTCTGATGAAGAAGTGGTAAATATCCAAAAGACCCCGTGAACTCT  
CGCATGACCGTTCGAGGGGAGCATACATAGAGAATGGATTTGCTATATCTGATCACTGTTTGAGCCG  
GAGGATCTAAGACGAGATGTGAAGAAATAAAACAGGTGACATTTTGTGAATGGATGGGTGCGAAGTCACA  
GGCTCAGCCCGAGGTGAGGCAATGGCAATTTGAAGAAGCAATCATCTCGATAGTACTCAAGCTTTGGAAGT  
CAAGATGATGAGCCCGCAAGGACTGAGCGAGCCGACCGAGCTGGACTCAACCAACATGCCCCACCGA  
GTGCTGTTGCCCATCTGCGGTCTGTCGGTGGAAATACCGAGTGTGTGATAACTGAAGAATATTGTAAT  
CGAAGAAACAAGCTGGAAGTCTGGGCTTCGCTGATGTAGGAGTTATGAAGATACAAATGAARACAAACCTTT  
TTTCAATCAATCCATTGTGAAGGAACAACGACATCAATGATGAAGAATAGATGTGGTGATCTTCTGT  
CTGTCAATGGTAGAAGTCAATGGAATGATACATGCTGCTGGCAGACATGCTGAAGAAGTCTAARGAAGA  
ATTACTTCACTATTGTTTCTGGCTCGGCATCTTTTAPAGATCAATGATGGGTCAAGAGAAACAGAAA  
TCACAATAGGCTAAGAGTTGAACACATATTTATCTTGCACTTTTATTTAAAGAAGAATACATGT  
AAAAATCGAGAAAAGATGATCATTAATGAAGAGCGAGTTACCTCAGAAAATGATTTCAAAAAAATTA  
AAACTCATGTTTCTTTCAGTGTGGAGGATTTCTCATTACTTCAACAATGTTTATATTTTCTATCAAT  
AAAAAGCCTTAAAAACCTAAAATGATGTTTGTATACCCCACTGAATCAAGCTGATTAAATTTAAATTT  
GGTATGCTGGAAGTGTGCAAGAGGTACATATGGCCATTTTAATTTACAGCTAAAATATTTTAAAAATGCA  
TTGCTGAGAAACGTTGCTTTTCATGAACAAGATAAATTTTTCAGAGGTAAA

**FIGURE 147**

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGC PDGCASLTAT  
APSPPEVSAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRS  
FKKINRALSVLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITSIKINRVDP  
SESLSIRLVGGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLL  
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVVRKVDEPGV  
FIFNVLDGGVAYRHGQLEENDRVLAINGHDRLRYGSPESAHLIQASERRVHLVVSQRVQRS  
PDI FQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHRE  
WDLPIYVISVEPGGVISRDGRIKTGDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEV  
KEYEPQEDCSSPAALDSNHNMAPPSDWSPSWVMWLELPRCLYNCKDIVLRNRTAGSLGFCIV  
GGYEEYNGNKPFFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHACLARLLKELKGRI  
TLTIVSWPGTFLL

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**FIGURE 148**

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT  
GCACAGGGCAGCTTTACTTACTCCAGCACCTTCTCTCCCAGGCAAATGTTGCTGACCATCT  
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC  
AATGTTGAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC  
AGGATCATGCTCTTCTACCACAATTTTGGACTATAAACATGGCTACATTGCATCCAGGGTGC  
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT  
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG  
GGTCAAGTACAACCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCTCGCTTGGGTCAC  
CCATTGAGAAACTCTGCAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT  
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG  
TGCAGACATTCATGTTTAGGATGATTAGCCCTCTGTTTTATCTTTTCAAAGAAATACATCC  
TTGGTTTACACTCAAAGTCAAATTAAATCTTTCCCAATGCCCCAACTAATTTTGAGATT  
AGTCAGAAAATATAAATGCTGTATTATA

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**FIGURE 149**

MKILVAFVLVLTIFGIQSHGYEVFNIIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT  
IFDYKHGYIASRVLRRACFILKMDHQNIPPLNNLQWYIYEKQALDNMFSNKYTWVKYNPLE  
SLIKDVDWFLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

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T09TT 2840660

GGCAGCAGCCAGGAACATAGGAGGTTCCTACTGCCGAGCAGAGGCCCTACACCCACCGAGGC  
**ATG**GGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCAG  
 GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCTGGAAGTTTTCCCAAAG  
 GCCGTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCCATCAGCTATTCCTC  
 TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGTGGTGAAGACCCACGAGCCGGCCTCCTT  
 CAACCTCAACGTCACTCAAGTCCAGTCCAGACTGCTCAGCTACTTCTGCCGGGCGTCTCT  
 CCACCTCAGGTGCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG  
 CCAGTGTCTGAGCTGCGGGCCAACTTCACTCTGCAGGACAGAGGGGCGAGGCCCGAGGGTGGA  
 GATGATCTGCCAGGCGTCTCTCGGCAGCCCACTATCACCAACAGCCTGATCGGGAAGGATG  
 GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCTCTGCG  
 AGCCAGACATCGGACTGGTTCCTGGTGCCAGGCTGCAAAAGACGCCAATGTCCTCAGCAGCCG  
 CCTCACAGTGGTGCCCCAGGTGGTGACCAAGATGAGAGCACTGCAGGCTCCCTTGAGA  
 GCCCATCTCTGCTTGCCTGTCTACAGGAGCACCCGCCCTGAGTGAAGAGGAGTTTGGG  
 GGGTTACAGGATAGGGAATGGGGAGGTCAGAGGACGCCAAGCAGCAGCCATG**TAGA**ATGAACC  
 TCCAGAGAGGCCAAGCAGCGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTCTGATTTGGA  
 GTTCATGCAAAATGAGTGTGTTTtagctgctctTGCCACAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 151**

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVPKGRWVLITCCAPQPPPPITYSL  
CGTKNIKVAKKVVKTHEPASFNINVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK  
PVSELRANFTLQDRGAGPRVEMICQASSGSPPITNSLIGKDGQVHLQQRPCHRQPANFSFLP  
SQTSDWFWCQAANNANVQHSALTVVPPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG  
GFRIGNGEVRGRKAAAM

**Signal Peptide:**

amino acids 1-18

**N-glycosylation Sites:**

amino acids 86-89, 132-135, 181-184

GGTCTCTTA**AATG**CAGCAGCGCCGCTACCAAGATCCTTCTGTGCCTCCGCTTCTGCTCCTG  
CTGTCGCGCTGGTCCC GGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGT  
CATCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAGA  
CTTTTCTTCACTATGACTGTGGCAACAAGACAGTACACCTGTCAGTCCCTGGGGAAGAAA  
CTAAATGTCAACAGCGCTGGAAAGCACAGAACCTCAGTACTGAGAGAGGTGGTGGACATACT  
TACAGAGCAACTGCGTGACATTACAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGC  
AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTTCAGT  
TTCGATGGGCAGATCTTCTCCTCTTTGACTCAGAGAAAGAAATGTGGACACCGTTCACTCC  
TGGAGCCACAAGATGAAAGAAAAGTGGGAGAAATGACAAGGTTGTGGCCATGTCTCTCCATT  
ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC  
CTGGAGCCAAAGTGCAGGAGCACCACTCGCCATGTCTCAGGCACAACCCAACCTCAGGGCCAC  
AGCCACCACCTCATCCTTTGCTGCCTCCTCATCATCTCCCTGCTTCATCCTCCCTGGCA  
TCTGAGGAGAGTCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCAG  
GTCTTGATCAAATCGCCCTTCTGTCTGGCCAGTGGCCACGACCTACGGTGATGTCCAGT  
GGCCTCCAGCAGATCATGATGACATCATGACCCAATAGCTCATTCAGTGCCTTGATTCTT  
TTGCCAACAAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC  
TGATGGAATTCCTGCACTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTC  
TCTTTTGTTTGGAAAATCAAGTACTTCTTTGAATGATGATCTCTTTCTGCAAAAGATATT  
GTCAGTAAATAATCAAGTTAGACTTACAGCTTCAGGGATCTTTCCGTGTCCTGAAGAG  
AATTTTAAATTTATTTAATAAGAAAAAATTTATATTAAATGATGTTTCTTTAGTAATTTAT  
TGTTCTGTACTGATATTTAAATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAAAAA



**FIGURE 153**

MAAAATKILLCLPLLLLLSGWSRAGRAPHSLCYDITVIPKFRPGPRWCACVQGQVDEKTF  
HYDCGNKTVTPVSPGLGKLNVTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR  
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFS  
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

**Important features:****Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 224-246

**N-glycosylation site.**

amino acids 68-72, 82-86

**N-myristoylation site.**

amino acids 200-206, 210-216

**Amidation site.**

amino acids 77-81

**FIGURE 154**

GGGAAAGCCATTTTCGAAAACCCATCTATACAACTATATATTTTCATTCTGCTGCTAGCTG  
CCTTGGGCCTCACAATTTTCATTCTGTTTTCTGACTTTCAGTTATATACCGTGGAAATGGAG  
TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTTGGTGGTAGCCCTCACCCAATTCG  
GTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAAATCATGAACCTCTGGCTGTTGATCAAAA  
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAAGAAGCTAGCAGAAGAC  
TCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAAATGGATTCTACAT  
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATGGGAGGCCAAC  
CCACAGAACAGCATTTCTGGGCCAGGCTGTAATCAGAATTGTCGTCGTACATGCTCAACAGC  
ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCCTTACCTTT  
CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAAACCTTGACGAAGGGACC  
TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATTTCTGTAT  
CATCCTTTTCAATAAACTGTATTCTATTTGAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 155**

MELIPTITSWRVLLLVVALTQFWCGFLCRGFHLQNHFWLLIKREFGFYSKSQYRTWQKKLA  
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGQPTEQHFWARL

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**FIGURE 156**

GTTCTCCTTTCCGAGCCAAAATCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATGAAG**  
 CTCTTGTGGCAGGTAACCTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTTCGTCTA  
 CCTCACGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCCCTCAGCCGGGGCCCC  
 AGAAGTCGCCCTCCGTTTGTCTGTGCAGTAACCAAGTTGAGCAAGGTGGTGTGCACGGCCGG  
 GGCTCTCCGAGGTCCCGCAGGGTATTCCCTCGAACACCCGGTACCTCAACCTCATGGAGAA  
 CAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCCTGCAGT  
 TGGGCAGGAACCTCCATCCGGCAGATTGAGGTGGGGGCCCTCAACGGCCTGGCCAGCCTCAAC  
 ACCCTGGAGCTGTTCCGACAACCTGGCTGACAGTCATCCCTAGCGGGGCCCTTGAATACCTGTC  
 CAAGCTCGGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCTCTTACGCCTTCA  
 ACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT  
 GAGGGAGCTTTTGGGGGCTGTTCACCTCAAGTATCTGAACCTTGGGCATGTGCAACATTAA  
 AGACATGCCCAATCTCACCCCCCTGGTGGGGCTGGAGGAGCTGGAGATGTCAGGGAACCACT  
 TCCCTGAGATCAGGCCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTCTAG  
 AACTCACAGGTCAGCCTGATTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAAC  
 CAACCTTGGCCCAACAATAACCTCTCTTCTTTGCCCATGACCTCTTTACCCCGCTGAGGTACC  
 TGGTGGAGTTGCATCTACACCACAACCTTGGAACTGTGATTGTGACATTCTGTGGCTAGCC  
 TGGTGGCTTCGAGAGTATATACCCACCAATTCCACCTGCTGTGGCCGCTGTCTGCTCCCAT  
 GCACATGCGAGGCCGCTACCTCGTGGAGGTGGACCAGGCCTCCTTCCAGTGCTCTGCCCCCT  
 TCATCATGGAGCGCACCTCGAGACCTCAACATTTCTGAGGGTCGGATGGCAGAAGCTTAAGTGT  
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTTGCTGCCCAATGGGACAGTGCTCAGCCACGC  
 CTCCCGCCACCAAGGATCTCTGTCTCAACGACGGCACCTTGAACCTTTTCCACGCTGCTGC  
 TTTTCAGACACTGGGGTGTACACATGCATGGTGACCAATGTTGAGGCAACTTCAAAGCCTCG  
 GCCTACCTCAATGTGAGCAGCGGCTGAGCTTAACACCTCCAACATACAGCTTCTTACCACAGT  
 AACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCCCTA  
 CCACGCTCCACTGGTTACACGCGGECATATACCACCTCTACCACGGTGCTCATTACAGACTACC  
 CGTGTGCCCAAGCAGGTGGCAGTACC CGCGACAGACACCACTGACAAGATGCAGACCAGCCT  
 GGATGAAGTCATGAAGACCACCAAGATCATATTGGCTGCTTGTGGCAGTGACTCTGCTAG  
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGGACACGACGCGGAGTACAGTC  
 ACAGCCGCCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCAGCAGCAACATCCCG  
 AGCAGCAACAGCAGCTCCGTCCGGTGTATCAGGTGAGGGGCGAGTAGTGCTGCCCAACATTC  
 ATGACCATATTAACTACAACACCTACAACACGACATGGGGCCCCTGGACAGAAAAACAGC  
 CTGGGGAAGCTCTCTGCACCCACAGTCACCACTATCTCTGAACCTTATATAATTAGACCCCA  
 TACCAAGGACAAGGTACAGGAACTCAATA**TGACT**CCCCCCCCCAAACTTATAAAAT  
 GCAATGAAGATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTTCTTGTA  
 TATGCTTATATATTAGTCTATGGGCTGGTTAAAAAAAACAGATTATATTAATAATTTAAAGA  
 CAAAAAGTCAAAACA

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**FIGURE 157**

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAASAGPQNCPSVCSCSNQFSKVVCT  
RRGLSEVPQGI PSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS  
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY  
ISEGAFEGLEFNLYNLGMCNIKDMPNLTPLVGLEELEMNGHFFPEIRPGSFHGLSSLKKLW  
VMNSQVSLIERNAFDGLASLVEINLAHNNLSSLPDHLFTPLRYLVELHLHHNPWNCDLW  
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFOCSAPFIMDAPRDLNISEGRMAEL  
KCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGT LNF SHVLLSDTGVYTCMVTNVAGNSN  
ASAYLNVSTAE LNTSNYSFFT VTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ  
TTRVPKQVAVPATD TTDKMQTS LDEV MKTKIIIGCFVAVTLAAAMLIVFYKLRKRHQQRS  
TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEGAVVLPTIHDHINYNTYKPAHGAHWTE  
NSLGNLHPTVTTISEPYIIQTHTKDKVQETQI

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**FIGURE 158**

CGCTCGGGACACAGCCGCGGCAAGGATGCGAGCTGGGTGCTGGACGCAGTTGGGGCTCAGTTTCTTCAGCTCC  
 TTCTCATCTCGTCTTGCACAGAGAGTACACAGTTCATTAAATGAAGCTTGCCTGGAGCAGAGTGGAAATATCATG  
 TGTGCGGAGTGCTGTGAATATGATCAGATTGAGTGCCTCTGCCCGGAAAGAGGGAAAGCTCGTGGGTATACCAT  
 CCCTTGCTGCGAGGAATGAGGAGAAATGAGTGTGACTCCTGCCTGATCCACCCAGGTTGTACCATCTTTGAAACAT  
 GCAGAGCTGCGGAAATGGCTCATGGGGGGGTACCTTGGATGACTTCTATGTGAGGGGTTTCTACTGTGCGAGAG  
 TGCCGAGACGGCTGCTAGCGAGGAGACTGCATGCGATGTGGCCAGGTTCTGCGAGCCCAAGGGTTCAGATTTT  
 GTTGCAAAAGCTATCCCTTAATGCTCAGTGTGATGGACATTATGCTAAACCTTGGGTTGTTCATCCAACTAA  
 GATTGTTCATGTTGAGTCTGGAGTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTGCTGATGGAGACAAC  
 CGCGATGGCCAGATCATCAAGCTGTCTGTGCCAAGCAGCGCCAGCTCCTATCCAGAGCATAGGATCCTCACT  
 CCAGTCTCCTTCCACTCCGATGGCTCCAAGAAATTTGACGGTTTCCATGCCATTATGAGGAGATCACAGCAT  
 GCTCCTCATGCCCTGTGTTCCATGACGGCAGCTGCCCTCTTGACAAGCTGGATCTTACAAGTGTGCCCTGCTTG  
 GCAGGCTATACTGGGCAGCGCTGTGAAATCTCCTTGAGAAAGAACTGCTCAGACCTCGGGGGCCAGTCAA  
 TGGGTACCAAGAAATACAGGGGGGCCCTGGGCTTATCAACGGACGCCATGCTAAATTTGGCACCCTGGTGTCTT  
 TCTTTTGTAACTCCTATGTTCTTAGTGGCAATGAGAAAGAACTTGCCAGCAGATGGAGAGTGGTCAGGG  
 AAACAGCCCATCTGCATAAAGGCTGCCGAGAACCAAGATTTGAGACCTGGTGAGAGGAGAGTTCTTCCGAT  
 GCAGGTTTCAAGGGAGACACCATACACAGCTATACTCAGCGGCCCTCAGCAAGCAGAACTGCAGAGTG  
 CCCCACCAAGAAGCCAGCCCTTCCCTTTGGAGATCTGCCATGGGATACCAACATCTGCATACCCAGCTCCAG  
 TATGAGTGCATCTCACCTTCTACCGCCGCTGGGCAGCAGCAGGAGGACATGTCTGAGGACTGGGAAGTGGAG  
 TGGCGGGGACCATCCTGCATCCTTATCTGCGGGAAATTTGAGAATCATCTGCTCCAAAGACCCAGGGTTGCT  
 GCTGGCGGTGGCAGGAGCCATCTACAGGAGGACAGCGGGGTGCATGACGCGAGCCTACACAAGGGAGCGCTGG  
 TTCTAGTCTGCAGCGGTGCCCTGGTGAATGAGCGCAGTGTGGTGGTGGCTGCCACTGTGTTACTGACCTGGG  
 GAAGTCCACATGATCAAGACAGCAGACTGAAAGTTGTTTGGGGAATTTACCGGGATGATGACCGGGATG  
 AGAAGACCATCCAGAGCCTACAGATTTCTGCTATCATTTGATCCCACTATAGCCCATCTGCTTGATGCT  
 GACATCGCCATCCTGAAGTCTCTAGACAAGGCCGTATCAGCACCCGAGTCCAGCCCATCTGCCCTGCTGCCAG  
 TCGGATCTCAGCACTTCTTCCAGAGTCCACATCACTGTGGCTGGTGGAAATGCTCCTGGCAGACGTGAGGA  
 GCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGGTGTGAGTGTGGTGGACTCGTGTGTGTGAGGAGCAG  
 CATGAGGACCATGGCATCCAGTGTGATGCTGATACATGTTCTGTGCGAGCTGGGAACCCACTGCCCTTCT  
 TGATATCTGCACTGCAGAGCAGGAGGCATCGCGGTGTGCTCTCCGGGAGCAGCATCTCCTGAGCCAGCT  
 GGCATCTGATGGGAGCTGGTCACTGTGAGCTATGATAAAACATGCAGCCACAGGCTTCCACTGCCCTCACCAAG  
 GTGCTGCCCTTTAAAGACTGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACTCCTTGAGAAGTGTTC  
 TGTATATCCGCTGTGACGTGTGCTGCTGAGCAGTGTGGGCTGAAGTGTGATTGGCTGTGAACTTGG  
 CTGTGCCAGGGCTTCTGACTTCAGGACACAACTCAGTGAAGGTTGAGTAGACCTCCATTGCTGGTAGGCTGAT  
 GCGCGCTCCACTATGAGACACCAATTTGGAAGATGCCAGGGCTTGAAGAAGTAACTTTCTTCAAGAGAGACC  
 ATATACAAACCTTCCACTCCACTGACCTGGTGGTCTTCCCACTTTCAAGTTATCAAGATGCCATCAGCTG  
 ACCAGGGAAGATCTGGGCTTCATGAGGCCCTTTTGGGCTCTCAAGTTCTAGAGAGCTGCCCTGTGGGACAGCT  
 CAGGGCAGCAGAGCTGGGATGCTGGTGCATGCTTTGTGACATGCCACAGTACAGTCTGGTCTTTTCCCTCC  
 CCATCTCTTTGTACACATTTTAAATAAATTAAGGTTTGGCTTCTGAACATCAAAAAAAAAAAAAAAAAAAAA  
 AA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 159**

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAERNIMCRECCEYDQIECVCPGKREVV  
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGD  
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD  
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDG  
TCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV  
VSFFCNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLH  
QLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK  
WSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNE  
RTVVVAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLD  
ADIAILKLLDKARISTRVQPICLAASRDLSFSQESHITVAGWNVLADVRSPGFKNDTLRSG  
VVSVDSSLCEEQHEDHGI PVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPR  
WHIMGLVSWSYDKTCSHRLSTAFTKVL PFKDWIERNMK

**FIGURE 160**

ACCAGGCATTGTATCTTCAGTTGTTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGA  
 AGCTTTCTTGCCCTGCAGTGAAGCAGAGAGATAGATATATTTCACGTAATAAAAAACATGGGC  
 TTCAACCTGACTTTCCACCTTTCTTACAATTCGATTACTGTTGCTGTTGACTTTGTGCTT  
 GACAGTGGTTGGGTGGGCCACCAGTAACTACTCGTGGGTGCCATTCAGAGATTCCCTAAAG  
 CAAAGGAGTTCATGGCTAATTTCCATAAGACCTCATTTTGGGGAAGGAAAAACTGACT  
 AATGAAGCATCCACGAAGAAGGTAGAACTTGACAACTGTCCTTCTGTGTCTCCTTACCTCAG  
 AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAATC  
 CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAGCTTTACAGAGGGTCGCCATC  
 CTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAACATCTGCATCCCTT  
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTATCCACCAGGCTGAAGGTAAAAAGT  
 TTAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAACCCCTCAAGGAAGAAAAATGGGAC  
 TGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA  
 GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG  
 GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT  
 AACAACTACTGGGGATGGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAG  
 AATGAAAATTTCCCGGCCCTGCCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAG  
 ACAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTACGAGTCTGG  
 AGAACAGATGGGTTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA  
 TATCAACATCAGAGTGATTCTGGTTTGGTGCATGACCCTGGATCTTTTGGTGATGTTTGG  
 AAGAACTGATTCTTTGTTGCAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA  
 AGAACCTGTTACAGCTCATTTGTTGAGCTGAATTTTCTTTTTGTATTTTCTTAGCAGAGCT  
 CCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGATCATG  
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT  
 AAAATGAACGCTATTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATAT  
 TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGCTGTGAGAGAACCAGAGTTGTTCT  
 CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTCATTTATCCTGTACAATCATCT  
 GTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCAGCAATCA  
 GGACACAGTGAACTTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGCGCTGCAAAAGGCAG  
 CAGTAGCTGAGCTGGTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCT  
 TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAAATGA  
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAACTAATAATAATA  
 TGCTATCAAATACCTCTGTAGTAAAATGTGAAAAGCAAAA

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**FIGURE 161**

MGFNLT FHLSYKFRLLLLLTLC LTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLILGKGKT  
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEE VQAENPKVSRGRYRPQECKALQRV  
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAE GKKFNRAKLLNVGYLEALKEEN  
WDCFI FHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVTALSREQFFKVNG  
FSNNYWGWGGEDDDLRRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR  
VWRTDGLSSCSYKLVSV EHNPLYINITVDFWFGA

**Important features:****Signal peptide:**

amino acids 1-27

**N-glycosylation sites:**

amino acids 4-7, 220-223 and 335-338

**Xylose isomerase proteins:**

amino acids 191-201

**FIGURE 162**

CGTGGGCGGGGTCGCGCAGCGGGCTGTGGGCGCGCCGAGGAGCGACCGCCGAGTTCTC  
 GAGTCCAGCTGCATTCCCTCCGCTCCGCCCCACGCTTCTCCGCTCCGGGCCCCGCAATG  
 GCCAGGCAGTGTGGTCGCGCTCGGCGGCATCCTCTGGCTTGCCTGCCTCCTGCCCTGGGC  
 CCGGCGAGGGGTGGCCGAGCCTGTATGAACTCAATCTCACCACCGATAGCCCTGCCACCA  
 CGGGAGCGGTGGTGACCATCTCGGCCAGCCTGTGGCCAAGGACAACGGCAGCTTGCCCTGG  
 CCCGCTGACGCCACCTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGCTTACTGGCAA  
 GATGGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTCGGCCACGTGCCCGGGGAATTCCCGG  
 TCTCTGTCTGGGTCACTGCCGCTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTG  
 GTCTCCCCATCACAGATTTCTCGTGGGGGACCTTGTGTACCCAGAACACTTCCCTACC  
 CTGGCCCAAGTCTTATCTCACTAAGACCGTCTGAAAGTCTCCTTCTCTCCACGACCCGA  
 GCAACTTCTCAAGACCGCCTTGTCTCTACAGCTGGGACTTCGGGGAGCGGACCCAGATG  
 GTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGACCTTCAACGTGAAGCT  
 CAAAGTGGTGGCGGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGA  
 CCGGGGACTTCTCCGCTCGCTGAAGCTGCAGGAAACCTTCGAGGCATCCAAGTGTGGGG  
 CCCACCTTAATTCAGACCTTCCAAAAGATGACCGTGACCTTGAACCTTCTGGGGAGCCCTCC  
 TCTGACTGTGTGCTGGCTCTCAAGCCTGAGTGCTCCCGCTGGAGGAAGGGGAGGTGCCACC  
 CTGTGTCCGTGGCCAGCAGCGTACAACCTGACCCACACCTTCAGGGACCTTGGGACCTAC  
 TGCTTCAGCATCCGGGCCGAGAATATCATCAGCAAGACACATCAGTACCACAAGATCCAGGT  
 GTGGCCCTCCAGAATCCAGCCGCTGTCTTGTCTTCCCATGTGTACACTTATCACTGTGA  
 TGTGTGGCTTATCATGTATACATGACCTGCGGAATGCCACTCAGCAAAAGGACATGGTGGAG  
 AACC CGAGCCACCTCTGGGGTCAGGTGCTGCTGCCAGATGTGCTGTGGGCTTTCTGTGT  
 GGAGACTCCATCTGAGTACCTGGAAATGTCTGTGAGAACCCGGGCTGCTCCGCCCCCTCT  
 ATAAGTCTGTCAAAACTTACACCGTGTGACCACTCCCCCTCCCCAACCCATCTCAGTGTAA  
 CTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAAGAGGGGTTCATT  
 TCGTGGGGCTTGTGGCCTGGATCCTCATCCATCTGTACAGTTTCCGCACTGCCACAAGCC  
 CCTCCCTCTGTGACCCCTGACCCAGCCATTACCCATCTGTACAGTTCAGCACTGCCACAAGCC  
 TAAGCCCCACTCGGTTACACCCCTTGACCCCTACCTTTGAAGAGGCTTCGTGCAGGACT  
 TTGATGCTTGGGGTGTTCGCTGTGACTCCTAGTGGGCTGGCTGCCACTGCCATTCCTCT  
 CTCATATTGGCACATCTGCTGTCCATTGGGGTCTCAGTTTCTCCCCAGCAGCCCTAC  
 CTGTGCCAGAGAGCTAGAAAGAGGTCTAAAGGGTTAAAATCCATAAGGTTGTATC  
 ACATAGATGGGCACACTCACAGAGAGAAGTGTGCATGTACACACACACACACACACACA  
 CACACACACACAGAAATATAACACATGCGTCACATGGGCATTTCAGATGATCAGCTCTGTA  
 TCTGGTTAAGTCCGTTGCTGGGATGCACCTGCCTGACTAGAGCTGAAAGGAAATTTGACCTCCA  
 AGCAGCCCTGACAGGTTCTGGGCGCGGCCCTCCCTTTGTGCTTTGTCTCTGCAGTTCTTGC  
 GCCCTTTATAAGGCATCTAGTCCCTGCTGGCTGGCAGGGGCTGGATGGGGGGCAGGACT  
 AATACTGAGTGATTCGACAGTGCTTTATAAATACACCTTATTTTATCGAAACCCATCTGTG  
 AAACCTTTCACGTAGGAAAGGCTTGCAGCGGTAGAAGAGGTTGAGTCAAGGCCGGGCGCGG  
 TGGCTCAGCCCTGTAAATCCAGCACTTTGGAGGCCGAGGCGGGTGGATCAGAGATCAGGAG  
 GATCGAGACCACCTGGCTAACACCGGTGAACCCCGTCTCTACTAAAAAATACAAAAAGTT  
 AGCCGGGCGTGGTGGTGGTGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCAGGAGAATG  
 TGCGAACCCGGGAGGCGAGCTTGCACTGAGCCAGATGGCGCCTGCACTCAGGCTGA  
 GTGACAGAGCGAGACTCTGTCTCCA

**FIGURE 163**

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA  
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVVVTAAADCWMCQPVARGF  
VVLPITEFLVGD LVVTQNTSLPWSSYLTKTVLKVSFLLHDP SNFLKTALFLYSWDFG DGTQ  
MVTEDSVVYYNYSIIGTFTVKLVVAEWEVEPE DATRAVKQKTGDFSASLKLQETLRGIQVL  
GPTLIQTFQKMTVTLNFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDPGD  
YCFSIRAENIISKTHQYHKIQVWPSRIQPAVFAFP CATLITVMLAFIMYMTLRNATQQKDMV  
ENPEPPSGVRCCQMC CGPFLETPSEYLEIVRE NHGLLPPLYKSVKTYTV

**Important features of the protein:****Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 339-362

**N-glycosylation sites.**

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

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**FIGURE 165**

MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH  
FPICIFCCGCCCHRSKCGMCCKT

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**FIGURE 166**

CTGTG CAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGC  
 CTGGATCTTCCACCATGTCTCTGTTGCTGCCTTTTGTATAGCCTGATTGTCAACCTTCTGGGC  
 ATCTCCCTGACTGTCCTCTTACCCCTCCTTCTCGTTTTCATCATAGTGCCAGCCATTTTGG  
 AGTCTCTTTGGTATCCGCAAACTCTACATGAAAAGTCTGTTAAAAATCTTTGCGTGGGCTA  
 CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCCAGCTTTTACAAGCCCTACACCAAC  
 GGAATCATTGCAAAAGGATCCCACCTTCACTAGAGAAGAGATCAAAAGAGATTCGTGCAAGTGG  
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCCAGCTCTCTGACATTTTCTACTTTTGGC  
 GGAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAAC TG  
 GAGTCTCTGGAACCTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC  
 GGTCTGTGGGGGTTAGGAGTGCTGATTCGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC  
 TGGCTTTTACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTGGTGGGATACCTTGCCAAAT  
 GGGAGGTTTAAGGAATTCATGAGTAAACATGTTTCACTTAATGTGTTACCGGATCTCGCTGGC  
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCT  
 GTGTGGCCAATCATACCTCACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC  
 ATGGTGGGTCAAGTGACAGGGGGACTCATGGGTGTGATTCAGAGAGCCATGGTGAAGGCCCTG  
 CCCACACGCTCTGGTTGAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA  
 CTGAACATGTGCAAGATAAAGCAAGCTGCCTATCCTCATCTTCCAGAAGGAACCTGCATC  
 AATAATACATCGGTGATGATGTTCAAAAAGGGGAAGTTTTGAAATTGGAGCCACAGTTTACCC  
 TGTGTCTATCAAGTATGACCCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAAATACGGGA  
 TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTG  
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAAATCTGC  
 CATTTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCTGAAGAGCGAGAAGG  
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGGAACCAC  
 AAGGACAGGAGCCGCTCCTGAAGCCTGCCTCCAGCTGGCTGGGGCCACCGTGCGGGGTGCCAA  
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCTTCTGCTTTTCCAGACTCCAGGG  
 CTCCCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTTCGCCGAGCCGAGCGGGATCCCTGT  
 GCACCCGGCGCAGCCTACCCCTTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCCAGCCAGGA  
 CGAGATGCCTTGTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAAGTGAACCTCCCA  
 CCTTTGCACGCTGTGCGGGCTGAGTGCTTGGGAGATGTGGCCATGGTCTGTGTCTAGAGAT  
 GCGGGTACAAGAGTCTGTTATGCAAGCCCCTGTGCCAGGGATGTGCTGGGGCGGCCACCCG  
 CTCTCCAGGAAGGCACACTGAGGCACCTGTGGCTCGGCTTCCGCTTCAACATCGCCCCAGC  
 CTTGGAGCTCTGCAGACATGATAGGAAGGAACTGTCTATCTGCAGGGGCTTTTACGAAAATG  
 AAGGGTTAGATTTTATGCTGCTGCTGATGGGGTTACTAAAGGGAGGGGAAGGCGAGGTG  
 GCGCGCTGACTGGGCGACTGGGGAGAACGTGTGTTCTGCTACTCCAGGCTAACCTGAACCTCCC  
 ATGTGATGCGCGCTTTGTTGAATGTGTGCTCGGTTTCCCCATCTGTAATATGAGTCGGGGG  
 GAATGGTGGTGAATCTTCACTCACAGGGCTGTTGTGGGGATTAAAGTGTCTGCGGGTGAGTGA  
 AGGACACATCAGCTTCAGTGTTCAGTACAGGCCCAACAAAGCGGGCACGGCAGGCTGAG  
 CTCAGAGCTGCTGCACTGGGCTTTGGATTGTTCTTGTGAGTAAATAAACTGGCTGGTGAA  
 TGA

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**FIGURE 167**

MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIVPAIFGVSGIRKLYMKSLLKIFAWATLRME  
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRS GSSKALDNTPEFELSDIFYFCRKGME  
TIMDDEVTKRFSAAEELESWNLLSRTNYNFYISLRLTVLWGLGVLIRYCFLLPLRIALFTG  
ISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRALTAITYHDRENRPNGGICVANH  
TSPIDVIIILASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ  
DKSKLPILIFPEGTCINNTSVMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYL  
LRMTSWAIVCSVWYLPMTREADEDAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTF  
KEEQQKLYSKMIVGNHKDRSRS

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**FIGURE 168**

GCCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCCACCCGGACCCCTGGCCCTCA  
 CGTCTCCTCCAGGGATGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCAC  
 ACCTGGCAGGCCAGGCTGTTCCCAACATCCTGCCCCCTGGGCCTGGCTCCAGACACCTTTGA  
 CGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG  
 AAATGGCCCAACATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCAGGAGACCTGGGAGGAC  
 AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGT  
 CTACACCAACTCATCGAACACCTTGTAAGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG  
 GCTCCCGGGAGCTCTACATGAGGCACCTTCCCTTCAAGGCCCTGCATTTCTACCTGATCCGG  
 GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTCCG  
 AGGTGTGGGCAGCCTTCGCTTTGAACCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT  
 TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCCAAGATTTGGGGAGAAGAGGCGGGGCTGT  
 GTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCTCCTCTCTGCCCCCTG  
 GAAGACTCTGCTCTTGCCCCCTGGAGAGTTCCAGCTCTCAGGGGTGGGGCCCTGAAGTCCA  
 ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG  
 CAGCCTTGAGAAGCAAGAACATGGTTCCGGACCCAGCCCTAGCAGCCTTCTCCCCAACAGG  
 ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACCTCTGCTATGTGATGGGGACTTCCT  
 GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA  
 TGGAGTTTATTAGGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

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MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEKAAPLLKEEAMAH  
ALLRESWEAAQETWEDKRRGLTLPFGKAQNGIAIMVYTNSSNTLYWELNQAVRTGGGSRRL  
YMRHFFPKALHFYLIRALQLLRSGGCSRGPGEVFRVGVSLRFEPKRLGDSVRLQGFASS  
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPWKTLTLLAPGEFQLSGVGP

**FIGURE 170**

GTGGCTTCATTTCACTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCAACATGCCTCA  
 CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG  
 GTCGGTTCGGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAGCAAGTTGACTC  
 TATTGTCTGGACCTTCAACACAACCCCTCTTGTACCATAACAGCCAGAAGGGGGCACTATCA  
 TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAG  
 CTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT  
 CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG  
 TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG  
 GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC  
 CCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT  
 GCGTTGCCAGGAACCCCTGTCAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT  
 GAAGGTGCTGCTGATGACCCAGATTCTCCTCATGGTCTCCTGTGTCTCCTGTTGGTGCCCT  
 CCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG  
 AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGGGAAACTCCTAACATATGCCCCCAT  
 TCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGACAATCCTAAAGGAAGA  
 TCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAAAGATGGAAATCCCCACTCAC  
 TGCTCACGATGCCAGACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGCAGTG  
 CACTCCCTAAGTCTCTGCTCA

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**FIGURE 171**

MAGSPTCLTLIYLWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT  
IQPEGGTIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV  
YEHLSPKVTMGLQSNKNGTCVTNLTCCMEHGEEVDVIYTWKALGQAANESHNGSILPISWRW  
GESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLCLLLVPLLLSLFVLGLFLW  
FLKRERQEEYIEEKKRVDICRETPNICPHSGENTYDTPHTNRTILKEDPANTVYSTVEIP  
KKMENPHSLTMPDTPRLFAYENVI

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**FIGURE 172**

CTGGTTCCCCAACATGCCTCACCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC  
TCTGGACCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGACTTTCCTCCCTGAAGTC  
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAC  
AGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA  
GATGGAGGCTACTCCCTGAAGCTCAGCAAAGTGAAGAAGTACTCAGGGATCTACTATGT  
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG  
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG  
ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT  
GGGGCAAGCAGCCAATGAGTCCCATATGGGTCCATCCTCCCATCTCCTGGAGATGGGGAG  
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCGTGCAGCAGAAACTTCTCAAGCCCC  
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCCTCCT  
GTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTCTTTGGTTTC  
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTGTGCGGAA  
ACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA  
TAGAACAACTCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAA  
AGATGGAATCCCCACTCACTGCTCACGATGCCAGACACCAAGGCTATTTGCCTATGAG  
AATGTTATCTAGACAGCAGTGCCTCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAA

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**FIGURE 173**

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCT  
GCTGTGTTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA  
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA  
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCTTGGAGAA  
TTCCTTAGTTCCTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG  
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT  
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAAACGAAAAGGATGGGGA  
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA  
GGTTTGCACAACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT  
GCCAATCGTCGCTCCAGGCCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTTGAGTGGAC  
ACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCCAGTATAAATTC  
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCAGTCTATCAACATGTTACC  
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCCCTTGACAAT  
TTTTCATGAAATTATTCTCTTCTCCTGTTCAATAAATGATTACCCTTGCACTTAA

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**FIGURE 174**

MKMLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ  
IHVLENSLVLKVHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI  
NEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

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**FIGURE 175**

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCAATGACCTGCTGCGAAGGATGGACATCCTGCAA  
TGGATTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG  
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTC  
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG  
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTTCATCATTTTTCAGTGTGATCA  
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTC  
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA  
CATTCATCCAGAATCCTTCAACTGTCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG  
GTTTCAATAAACCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTCCAC  
TTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTTTAGGTCTATTGCT  
TGTTGGAATTCTGGAGGTCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTC  
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTA  
TCAGTAGTTTGAAAAAAAAA

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**FIGURE 176**

MTCCEGWTS CNGFSL LV LLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA  
IPATTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCLISIQALLKGPLMCNSPSNSNA  
NCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHF DSEENKHRL  
IHFSVFLG LLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

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**FIGURE 177**

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCT  
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCT  
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC  
CAAGTTGCCAACTTAATCCACCTCCAGAAGCTCTTGACGCCAAGTTGGAAGTGAAGCACTG  
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAATTAGTGAA  
AAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAGTCTTTCAACGACACC  
CTGATCTTCACTAAAAATGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCTGC

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**FIGURE 178**

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNQLQVAKLNPPPEALAAKLEV  
KHCTDQISFKKRLSLKKSWWK

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**FIGURE 179**

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG  
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG  
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTC  
GAACTGTGACATGGGAGAGAGTGACCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG  
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG  
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG  
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC  
TCATCACTCCAGGCTCTGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA  
AGCCTAACTGGCCCCAGCACCTCCTCCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC  
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAACTCG  
CCCCACCACCCCTCA

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**FIGURE 180**

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCK  
YKSSQKQHSPVPEKAIPLITPGSATTC

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**FIGURE 181**

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGG**ATG**TCGCTGCTGAGCCGTGCC  
 TGGCTGGGCCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC  
 CTGGCTACTGCGCCGCATCCTGGCTTGGACCTATGCCCTTCTATAACAACGTGCCGCCGGCTCC  
 AGTGTTTCCACAGCCCCAAACGGAACGTGGTTTTGGGGTCACCTGGGCCTGATCACTCCT  
 ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCAGGGCTTTACGGT  
 ATGGCTGGGTCCCATCATCCCCTTCATCGTTTTATGCCACCTGACACCATCCGGTCTATCA  
 CCAATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGG  
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGAC  
 GCCCGCCTTCCATTTCAACATCCTGAAGTCTATATAACGATCTTCAACAAGAGTGCAAACA  
 TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAG  
 CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG  
 TCAGGAGAGGCCAGTGAATATATTGCCACCATCTTGAGAGCTCAGTGCCCTTGTAGAGAAAA  
 GAAGCCAGCATATCCTCCAGCACATGGACTTTCTGTATTACCTCTCCCATGACGGGCGGCGC  
 TTCCACAGGGCCTGCCGCTGGTGCATGACTTCAACAGACGCTGTCATCCGGGAGCGGCGTCG  
 CACCCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG  
 ATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCAGATGAGGAT  
 ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC  
 TGGGTCTGTACAACCTTGCAGGCCACCCAGAATACCAGGAGCGTGCCGACAGGAGGTGC  
 AAGAGCTTCTGAAGGACCGCATCCTAAAGAGATTGAATGGGACGACCTGGCCAGCTGCC  
 TTCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCG  
 ATGCTGACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC  
 TCATCGATATTATAGGGGTCCATCACAACCAACTGTGTGGCCGGATCCTGAGGTCTACGAC  
 CCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCCTTTCTC  
 CGCAGGGCCAGGAAGTGCATCGGCGAGGCGTTCGCCATGGCGGAGATGAAAGTGGTCTCTGG  
 CGTTGATGCTGCTGCACTTCCGGTTCTTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAA  
 TTGATCATGCGCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCGTAATGTAGGCTTGCA  
 G**TGA**CTTTCTGACCCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGGTGTGTCAAA

**FIGURE 182**

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPQPCKRNWFWG  
HLGLITPTEEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLF  
IRFLKPWLGE GILLSGGDKWSRHRRLT PAFHFNILKSYITIFNKSANIMLDKWQHLASEGS  
SR LDMFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY  
LSHDGRRFHRACRLVHDFTDVIRERRRTLPTQGIDDFKDKAKSKTLD FIDVLLSKDEDG  
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLA RHPEYQERCQEVQELLKDRDPKEIEW  
DDLAQLPFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW  
PDPEVYDPFRFDPENSKGRSPLAFIPFSAGFRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT  
EPRRKLELIMRAEGGLWLRVEPLNVGLQ

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**FIGURE 183**

CAACAGAAGCCAAGAAGGAAGCCGTCTATCTTGTGGCGATCATGTATAAGCTGGCCTCCTGC  
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCCCTCTCCTTGACTCCAGGGA  
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACCTCGGAGGAGCTAGAAA  
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAAGAGGGGATATTCTCAGG  
AAAGCAGACTCAAGTACCAACATTTTAAACCCAAGAGGAAATTTGAGAAAAGTTTCAGGATTT  
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTTGCCAGAATCTGGAACCATACA  
AGAAACGTGAGACTCCTGATTGCTTCTGGAAATACTGTGTCTGAAGTGAAATAAGCATCTGT  
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTTGAAAC  
AGTGTGGAGAAAAACTAGGCAAACTACACCCTGTTTCATTGTTACCTGGAAAATAAATCCTCT  
ATGTTTGCACAAAAAAAAAAAAAA

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**FIGURE 184**

MYKLASCCLLFTGFLNPLLSLPLDSREISFQLSAPHEDARLTPEELERASLLQILPEMLGA  
ERGDILRKADSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

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**FIGURE 185**

GAACATTTTGTAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT  
GGGGTTGCTGGTTTAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA  
CCACCTCCGCCAGGAAGTGCAGGCCCCACCTGTCTGCAACCCAGCTGAGGCC**ATG**CCCTCCCC  
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT  
CCAGCTTCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA  
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGGAAGATGGAGGTCAAGCAGA  
AGGGGCAGAGGATGAAGTGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT  
CAGGGGTTCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG  
GAAGAGGCCAAAGAGGCCCCAGCCGACAAG**TGA**TCGCCCACAAGCCTTACTCACCTCTCTCT  
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTA  
CAAGCTCAGGAGCGAATAAATGTTCAAAGTGA

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**FIGURE 186**

MPSPGTVCLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG  
GQAEGAEDLEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

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**FIGURE 187**

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCCTCGTCCAGTACCTC  
 GTGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGGTGCTGT  
 TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCTGATAGTCGTGATCATCGGGATGCTCGTG  
 CTCCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT  
 GAGTATGTCCCCACCCTAAGCCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATC  
 TTACACCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCACGCCCTGGGGCCAGAGTCTTT  
 GTCCCCCGTGTGCGCATGTGTTCAAGGTCAGCCTCTCCAGAAGTGAGATCATGGACAAAA  
 GGGCAAATCACAGGAAGAAATTAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC  
 TCACGCCGAGACCTGCAGGAGTGGTGCCAGTGCTTGAAGTAACAAGTTTAAATGTTTACA  
 GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT  
 CCAAAAACACAAGTAGAAATTCTAACAAATGAAATATATTACAGGCAGGTACCCACTAACCA  
 AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGT  
 AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT  
 AACAAACAACCTCCCTGCTCCTGGCACCAGCCGTTTTTGGTTCATGGTGGGCCAGCTGCAAGCG  
 TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGTTTCTGTGGAC  
 ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA  
 ACCCTTGGTCAGGGCAGAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGA  
 GCATCCCCCTGCCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCACCAAGA  
 GCCTCCTTGTTTACATAACACAGGTTACCCTACAAACCACTGTCCCCACACAACCTGGGGAT  
 GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCCTGAGGGTTGA  
 ATTTTTTTTAAATGAAAGTGAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA



**FIGURE 189**

GGAGTGCAGATGGCATCCTTCGGTTCCTCCAGACAAGCTGCAAGACGCTGACC**ATG**GCCAAG  
 ATGGAGCTCTCGAAGGCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT  
 ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG  
 TGCCCAAGCCCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCTGT  
 GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATACAACCTGGGAGACTGGGGATGA  
 CCGGTTCTCCTTCGGAGCTTCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAG  
 AACCAGGGGAGAGGTGCCAAGTTTCATTGAACCTACACCACCAGCCAAGAGAGGTGAGAAA  
 GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTCACCCCACTCTCCGATTTGGAGGGAA  
 GCGGTTGATGGAGAAGGCTTCCCTCCCTCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTA  
 TGGTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTCACTCAGCTTCTCCTGTCT  
 ACTAACAGACTTGCTACTCACTGGGAACCTGCCTGTGGGCTCAAACCTGAGCGCCTTTGCTG  
 CTGTTTCTCTGTCTGTCTGAGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAAGTC  
 TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGAATTATGGCTG  
 GGCTTCTACATGGCCTGGCTCTCCTTCACCTGCTGCATGGCGTGGCTGTCAACCACTTCA  
 ACACGTACACCAGGATGGTGCTGGAGTTCAAAGTCAAGCA**TAG**TAAAGAGCTTCAAGGAAAAC  
 CCGAACTGCCTACACATACCATCAGTGTTTCCTCGGGGCTGTCAAGTGCAGCCCCCAC  
 CGTGGGTCTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG  
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGATTTCAAAGAGGGGCCAGCCAGGAGCTG  
 AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTAGGAGTTAAGCGGGTTTGGGA  
 TAGGCTTGAGCCCTACCTTACAGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG  
 TCTCTTGAGCATGGTTTTTATAGAGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC  
 CTAAGGATTCCTGGGTGCCACTGCTCTCTTTTCTCTACAGCTCCATCTTGTTCACCCAC  
 CCCACATCTCACACATCCAGAATTCCCTTCTTTACTGATAGTTTCTGTGCCAGGTTCTGGGC  
 TAAACCATGGAGATAAAAAGAAGAGTAAATACACTTCCCGACCTTAAGGATCTGAAA

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**FIGURE 190**

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP  
VSLDGDNTSTQEYVQYNWETGDDRFSSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR  
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQL  
PPATNRLATHWEPCLWAQTERLCCCFLCPVRS PGDGGPHDVFTSLPSCQLGSRRLTTTCLE  
LWLGLLHGLALLHLLHGVGCHHLQHVHQDGAGVQVQA

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**FIGURE 191**

AACCTGGAAGGAAAGAAAGAAAGGTGACGCTTTGGCCCA**CATG**TGGTTACCCCTTGGTCTCCTG  
TCTTTATGTCTTTCTCCTCTTCCATTATTCTGTGCATCTCCCTCACTTAAGTCTCAGGCCGTGCA  
GCAGCTCCTGTGGACATTGCCATCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG  
TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTG  
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG  
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTGCCTGCCCTATTCTCTCTCCCAA  
GTCTGTTCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAG  
CAATCTGTGTGGTAGTGGGAGATTACCATGCAAGCCCCAGAGAAATGGAGGAGCTTTGT  
AGCCACCTCCTGTGCAGCCAGTATTAAATGTCCCTTCCCCTGCCCGCCGTAGATTGAG  
GACATTGCCCTCTGTGTGCCACCAACCAGGACTTTCCCTTGGCTTGGCATCCCTGGCTCT  
CTCCTGGTACCCAGCAAGACGCTCTGTTCCAGGGCAGTGTAGCATCTTTCAAGCTCCGTTACT  
ATGGCGATGGCCATGATGTTACAATCCCCTTGCTGAATAATCAAGTGGGAAGGGGAAGCA  
GAGGGAAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCTTGAGGAAAAACCAA  
GGGAAGCAACAGGAACCTCTGCAACTGGTTTTTATCGGAAAGATCATCTGCCTGCAGATGC  
TGTTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTCAGGTGTGTAAGGAA  
ATAGAACAGTCTGCTGGGAGTCAGCACTGGAATTCTGATTCACCAACTCTTTATTACTTTGGG  
AAGTCACTCAGCTCCTCCCGTAGCCATCTCAGGGTGACGGAACCCAGTGATTACCTGCTGG  
AACCAAGGAAACTAACATGTAGGTTACTAGTGAATACCCCAATGGTTTTCTCCAATTATGCC  
ATTGCCACCAAAACAATAAAACAAATTTCTCTAACACTGAAA

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**FIGURE 192**

MWLPIGLLSLCLSPILSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGME  
HRNHLCFCDLYDRATSPPLKCSLL

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**FIGURE 193**

GTAGCGCGCTTGGGTCTCCCGGCTGCCGCTGCTGCCGCGCGCGCTCGGGTCTGGAGCAGGAGCGACGTCA  
 CCGCC**AT**GGCGAGGCATCAAAGCTTTGATTAGTTTGTCCCTTTGGAGGAGCAATCGGACTGATGTTTTGATGCTT  
 GGATGTGCCCTTCCAAATATACACAAATACCTGGCCCTCTTTGTTCTATTTTTTACATCTTTACCATCTTCC  
 ATACTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTGTAAAGAACTTGCCATCTTTC  
 TTACAACGGGCACTTCTGCTGACGCTTTTGGACTCCCTATTGTTATTTGCCAGAGCACATCTGATTGAGTGGGA  
 GCTTGTGCACTTGTCTCACAGGAAACACAGCTCATCTTGCACCTATACTAGGCTTTTTCTTGGTCTTGGGA  
 CAATGACGACTTCAGCTGGCAGCAGTGG**CTGA**AAAGAAATTA**CT**GAACATTGTTCAAAATGGACTTCTGTCAATT  
 GTTGGCCATTACGGCACACAGGAGATGGGGCAGTTAATGCTGAATGCTATAGCAAGCCTCTTGGGGTATTTTA  
 GGTGCTCCCTTCTCACTTTTATTGTAAGCATACTATTTTCACAGAGACTTCTGAAGGATTAAGAGATTTCCT  
 CTTTTGAAAAGCTTGACTGATTTCACACTTATCTATAGTATGCTTTTTGTGGTCTCTGCTCAATTAAATAT  
 TTAGTGTTTTCTGTTAGTTGATTTTTTTTGGAAATCAATATGCAATGTTAAACACTTTTTAATGTAATCA  
 TTTGCATTGGTTAGGAATTCAGAATTCGGCGGGCTATTACTGGTCAAGTACATCTTTTCTCTTAAATATTAT  
 TAGCCTCCATTATTACAAAAAATTATAAAAATAAGTTTTCACTCAGTCAGGATGACATCACTCCCAATGTTATG  
 CAGACATACAGACGGTTGGCATACGTTATAGACTGTATACTCAGTGCAAAATATAGCTGCATTTATACCTCAGAG  
 GGGCCAAGTGTTAATGCCCATGCCCTCCGTTAAGGGTTGTTGGTTTTACTGGTAGACAGATGTTTTGTGGATTG  
 AAAATTTATTTATGGAATTGCTACAGAGGAGTGCTTTTCTTCTCAATTGTTAGAAGAATTTATGTTAACTTTA  
 AGGTAAGGGTGTAAAAACATTTTGAGATAAGTTTTTATTATGTTTATTATGTTAGAGTGAGTTGCAATGT  
 GGGAGAAGATGACATTGAATTCAGTTTTTGAATCCTGTTCTATTATTAAGTGAAATTTGIGATCTCCTATC  
 AACCTTTCATGTTTTACCTGTTAAATGGACATACATGGAACCACTACTGATGAGGGACAGTTGTATGTTTGC  
 ATCATATATGCCAGAAAACCTTCTCTGCTTCTCCTTTTGACTTATTTGGTATGTTGTATATATACATAAAA  
 TAACCTTTTCAATATAGTTTAAATACACTTAGAAGTGTTTACTTACCTGGAATAATGCTATGCCGTACAT  
 CAGAGTGCCCCCTCCCTGCAAGGCTTGCCATGATTAAACAGTAACCTGTTAGTCTTACAGATAATTCATGCA  
 TTAACAGTTTTAAGATTAGACCATGGTAATAGTAGTTCTTATTCTTAAGGTTATATCATATGTAATTTAAAG  
 TTTTATTAAGACAGTTTCTGTATACCTCTGAACCTGTTTGATTTTGAAGTTTCATCATGATAGATCTGCTTT  
 CCTTATAAAGGCATTTTGTGTGAGTTAATGCAAGTAGCCAACTCCAGCTATATAGCAGCTTCAGAAACAT  
 ACCTGACCAAAAAAATTCAGATAACAGGCATGATCAATTTATAGTGGTCTTTTACATCTAATAATTTACAGGA  
 CTTTTTTCAGGAGTGGGTTATAAAAAATTCAAGTTGGTCTGACAGTATTTTGTAAAGGATATTTGTTGTATG  
 TTTTATCAGTATACTTACATAAAAAATTTTCGCCATCAGCCAAAACCTCAGTAATCATGACAGCTGTCTGTTGT  
 TTTATGAGTTTATTCTCAAGAAAATGGGAATAAATTTGGGATTGTTGAGCTTTTTTACTAAAGATGCCATAA  
 AGCCACAGCTTTTATTGCCTAACCTTAAGCCATGACTTTTATAGATATGAGATGACGGGAAGCAGGACGAATATCG  
 GCGTGTGGCIGAGCCTTCCOACTGGAGGCTGAAGTGGCTTGTGGTATTATAAATGTTAGATTTCAGATTTCAGAGGAA  
 GGTGCAGGTACACATGAGTTAGACAGCTGGTGACACAGTTGGGAACCTTTTGTGCTGTGATCTACTGGACTTT  
 TTTTTGAGGAAGTGCATTCTCTGCTCTTCCCTATTTTCTGTTCTGGATGTCAGTGCAGTGCATGCTGACTG  
 TTTTATCCACTTGGCCACAGACTTTTCTAACAGCTGCGTATTATTTCTATATCAATTTGCAATGCTGCACTG  
 GTGCTTGTACCTTGATACTAGCTTGACATAGTGTCTCTGATTCTAGGCTAGTTACTTGAGATATGAAT  
 TTTCCATAGAATATGCATGATACAACATTAACCTTCTCTATGGAAGAAACCTTTTATGATGAACATAA  
 AGATTTTAAATATCTATTTTAAAAA

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**FIGURE 194**

MAGIKALISLSFGGAIGLMFLMLGICALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAM  
SNACKELAIFLTGTGIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSND  
DFSWQQW

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CCACCGAGCTTCGCCCGACCGGTCGCGCCACGCGTCGCGACAGCTTCGCCCGACGGCTCCGCGACCGCTCCGCG  
CAGCGCTTCGCCCGCGAAGCTTCGCCCGACGAGTTCGCGCGAGGAGGAAGAGCCGGCGGCGCTTCGCGCGCTCCG  
TCTCGAGCTTCGCCCGCGCGAATGGCAGCTGTTTCGCGCGAGTAAAGAGTCGAGCGCGGTCACTGTCGTGTTT  
CAATCAGCGGACGATTAACCAAGCATCTGCAGATCTCGTGGGGATCCGCGAGCCCGAGTTTGGAGTTTTCGCCCCAC  
AAGCTCAGCAGTCCGAATTCAGAGGAAAGGAAGGCGGAGGAGGGAAGCTTCGCGCTTCGCCGACGATTTGG  
GAAACTTCGCGGCTTCAGAAAGTCGCTCCCGCTTCGCCCGCGCGCTTCGCGCGCGAATTCGCGCGCGGCTTCCTC  
GACAGACTTTCGCGCTTCGCGATTCGCGCGAGTTCGCGCGAGTTCGCGCGAGTTCGCGCGAGTTCGCGCGAGTTCCTC  
GCGCTGCATATATGCTGATGACATTCGCGAGTTCGCGAGTTCGCGAGTTCGCGAGTTCGCGAGTTCGCGAGTTCCTC  
CTCTCTTACTACTGTGCTGAGGAGGAGCTTCGCGGCGGCTTGTGTGTGCTGCTGGGGCGCTGCTTCAGATGCT  
GCCCGCGCGCCCCGAGCGGCTGCCCGCACTGTCGCGCTCGAGGGCGCGCTGTGATCTGGAGGGCGCTCAAC  
CCACCGAGCGCCCCAACCTCTTCGCGCTGCTGGGCTTGTCTCTCGCTACGACAGCTCTTCGCGAGCTTCGCG  
GCGCGCGATTCACCGGGGTAAATGCACTCAGCTGGCTCTATCTGATACATCTCACTGCTGCTGCTGCTGCTG  
GGAGCGCTTTCAGAAATCGCGCGAGTTAAGAAATTCGCGCGAGTTCGCGCGAGTTCGCGCGAGTTCGCGCGAG  
GCTTCGCGCGAGTTCGCGCGAGTTCGCGCGAGTTCGCGCGAGTTCGCGCGAGTTCGCGCGAGTTCGCGCGAGTTC  
CTCTCTCAGCGCTTCGCGAGCTCACCACTGCTGATTCGCGGCGCAACGCCATCAGTTTGTGCCGCTGCGCAT  
CTTCAGGACTTCGCGCGAGCTCAAGTTTCTGCATTCGATGACATCAGTCAAGACTTCGCGCGCGCTTCCTTC  
TCCGCGGCTTCCTTAACTCAGCGATCGACCTCGACCTCGAGCAACGATCTGGTCAAGTTGAACTTCGCCACTTC  
CCGCGCTGATCTTCCTGCACTGCTGCTGCTGGGAGGACCAAGTTGGCATTTGTGTGCTGCTGCTGCTGCTGCTG  
GGTTTGGAACTTCGAGAAATGAGCTTCGCGCGACGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC  
TGGCGCACTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC  
CTCTCTCAGCGCTTCGCGAGCTCACCACTGCTGATTCGCGGCGCAACGCCATCAGTTTGTGCCGCTGCGCAT  
CTTCAGGACTTCGCGCGAGCTCAAGTTTCTGCATTCGATGACATCAGTCAAGACTTCGCGCGCGCTTCCTTC  
TCCGCGGCTTCCTTAACTCAGCGATCGACCTCGACCTCGAGCAACGATCTGGTCAAGTTGAACTTCGCCACTTC  
CCGCGCTGATCTTCCTGCACTGCTGCTGCTGGGAGGACCAAGTTGGCATTTGTGTGCTGCTGCTGCTGCTGCTG  
GCTTGGAAAGCGGCTGTAGCTCTTCACTTCGCGAGGATGAGGCGCGAGCCACAGCGCGCACTGCTCTCGCC  
CTCACCAACCGCATGATCTGGGCGCGCTCGGACCTTCGCCCGCACCGCTTCGCGGACGCGCGGAGGCGGACG  
CGACGCGCATTCAGTTCGCTGCGACCTGGCTTCGCGCGCGGAGTTCGCGCGAGTTCGCGCGAGTTCGCGCGAG  
AAGTTGCTTCAGCGCGCTTCGCGCGAGTTCGCGCGAGTTCGCGCGAGTTCGCGCGAGTTCGCGCGAGTTCGCGCGAG  
CTCTCTCAGCGCTTCGCGAGCTCACCACTGCTGATTCGCGGCGCAACGCCATCAGTTTGTGCCGCTGCGCAT  
CTTCAGGACTTCGCGCGAGCTCAAGTTTCTGCATTCGATGACATCAGTCAAGACTTCGCGCGCGCTTCCTTC  
TCCGCGGCTTCCTTAACTCAGCGATCGACCTCGACCTCGAGCAACGATCTGGTCAAGTTGAACTTCGCCACTTC  
CAGTGGCTCTCAACCATGCTCTACCAATAGCTCTGGGACGCGGAGCGGCGCGGCGCGCGAGCTTCGCGCGCTTC  
CTCTCTGCTGCTGCTCTGATATGCTCTTGAATGAARCTTAAAGGGATCTCTCTCGAGAGCTTCGCGCGAGTTC  
TTTATTTGCTCTTAAAGCAAAAGAGCTGATTAAGACATTAAGACATTAAGACATTAAGACATTAAGACATTAAG  
AAGTTGCTTAAAGCAAAAGAGCTGATTAAGACATTAAGACATTAAGACATTAAGACATTAAGACATTAAGACAT  
TAAAGTTGCTTAAAGCAAAAGAGCTGATTAAGACATTAAGACATTAAGACATTAAGACATTAAGACATTAAGACAT  
CCACAGAGGCTCTTAATCTCATTTGCTGCTATCTGAAAGAACTTAAAGGCGCAACTTCAGCTCTGCTGCTGCTG  
GGCATTTGATGATGATTAAGCTTGAACCTTTCGATCTCTTCCAGCTGATTAAATTCAGAGTTCGATTTAGGTT  
TTTTCGATATTTATAGAAAAGAGCTCTTTCAGATGACAAATGACATCTCACCTCAGCTTCAGATTCAGATTCAG  
GCTTTCGATGCTTTCAGATTCGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG  
CCCTTCAGCTTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG  
TTCGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAG  
TCTCTGAACTCATCAAGATTAAGAGAGCCCCAACCTTTCTCTGCTCTCAGAGAGAGACAGCATTTGATATG  
ATTTCAGATCATCAACACATATTTATGATATATAGTATACAGAGGCGCAATGCCATCTGTTATTTCTCTCCGA  
AGTTTTCAGAGACATCAACACATGATCTCTGATAGGAGTTCAGGCGGCTTGTGTTTCGCGCTTTTTCGATTAAG  
CTCTGTCAGAGACTTTGATGCTGAGTCTTCGATGATCTTCGATGATTCGATGATTCGATGATTCGATGATTCGATGAT  
GGTGAAGAGACATCATCAGTTCAGGCTGATCAAAATAAATTAATTTCTCTGATGATGATGATGATGATGATGATGAT  
GCTGATTTGGGCTGCTGATTCAGAGATTCGATTAAGAGAAATAGTTCAGATGATGATGATGATGATGATGATGATGAT  
CTGAATATTTTTCGATGATTTTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT

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**FIGURE 196**

MDFFLLGLCLYWLRLRPSGVVLCLLGACFQMLPAAPSGCQQLCRCEGRLLYCEALNLTEAPH  
NLSGLLGLSLRYNSLSELRAQQTGLMQLTWLYLDHNHICSVQGDAPQLRRVKELTSSNQ  
ITQLPNTTFRPMENLRSDLSYNKLQALAPDLFHGLRKLTLTHMRANAIQFVVPVRFQDCRS  
LKFLDIGYNQLKSLARNSFAGLFKLTTELHLEHNDLVKVNFAHFPRILSLHSLCLRNRKVAIV  
VSSLDWVWNLEKMDLSGNEIYEMPHVFETVPHLQSLQLDSNRITYIEPRILNSWKSLSITSIT  
LAGNLDWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDAVYAFHLCEDGAEPTSG  
HLLSAVTNRSLDGLPPASSATTLADGGEGQHDGTFEPAVALPGEHAENAVQIHKVVTGTMA  
LIFSFLIVLVLVYSWCKFPASLRQLGRQCFVTVQRRKQKQKQTMHQAAMSAQEYYVDYKPNH  
LEGALVINNEYGSCCTHOOPARECV

FIGURE 197

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**FIGURE 198**

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE  
GHAUSDMLLPDGLVLSAGAGFVSDVGSHLDCGAGEPAVFRDSDRFSWHDPHLWRSGDEA  
PGLFFVDAERVPCRHDDVFFPPSASFRVGLGPGASPVVRVRSISALGRTEFTRDEDLAVFLASR  
AGRLRFHGPGLSVGPEDCADPSGCVCGNAEAQPWICAALLQP

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**FIGURE 199**

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTT  
TGAGCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCTGTGTT  
CTGCCTTTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTTGCAGTCTTTGGCA  
TTGACGTGGTACAGCCTTTCCTTCATACCATTTGCAAGGGATGCTGTGAAGAAGTGTTTTGC  
CGTGTGCTTGCATTAATTTCATGGCCAGTTTTATGAAGCTTTGGAAGGCATATGGACAGAAG  
CTGGTGGACAGTTTTGTAACTATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCT  
TGCAGCAATGTGTTGCTTGTGATTTCGAACATTTGAGGGTTACTTTTGAAGCAACAATACAT  
TCTCGAACCTGAATGTCAGTAGCACAGGATGAGAAGTGGGTTCTGTATCTTGTGGAGTGGAA  
TCTTCCTCATGTACCTGTTTCCTCTCTGGATGTTGTCCCACTGAATCCCATGAATACAAAC  
CTATTACAGCAACAGCAA  
AAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 200**

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGGLALIFCILQSLALTWYSLSFIP  
FARDAVKKCFVCLA

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**FIGURE 201**

TTGAGCGCAGGTGAGCTCCTGCGCGTTCGCGGGCGGTTCTCCAGTCAACCCTCCGCGGTTACCCGCGGCGCGC  
 CCGAGGGAGTCTCCTCCAGACCCCTCCCTCCCGTTGCTCCAACTAATACGGACTGAACGGATCGCTGGGAGGGT  
 GGGAGAGAAATTAGGGGGAGAAAGGACAGAGAGCACTACCATCCATAGCCAGATAGATTATCTTCACTG  
 AACTGATCAAGTACTTTGAAATAGCACTTCGAAATTTATCTTGGTGTCTCTCATACTTGTCTGACTGAGTCTTTC  
 AACCACCTTTTCTCTCCAACTAGACCAGCAAAAGGTTCTACTAGTTTCTTTTGTGATTCCGTTGGGATTACT  
 TATATAAAGTTCCACGCCCCATTTTCATTATATTATGAAATATGGTGTTCACGTGAAGCAAGTTACTAATGTT  
 TTTATTACAAAAGCTCCCTAAACCATTATACTTTGGTAACCTGGCCCTTTGCAGAGAATCATGGGATTGTTGC  
 AAATGATATGTTTGATCCTATTTCGGAACAAATCTTTCTCTCTGGATCAGATGAATATTATGATTCCAAAGTTTT  
 GGGAGAGCGACACCAATATGGATCACAACCAGAGGGCGAGACATACTAGTGGTGCAGCCATGTGGCCCGGA  
 ACAGATGTAAAAATACATAAGCGCTTCTCTACTCATACATGCCTTACATAGTCAAGTTCATTGTGAAGATAG  
 AGTTGCCAAATTTGTTGAATGGTTTACGTCAAAGAGGCCATAAATCTTGGTCTTCTCTATTGGGAAGACCTG  
 ATGACATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGGCTGTCACTTTCAGATATTGACAAGAGCTTA  
 GGATATCTCATACAATGCTGAAAAGGCGAAAGTTGTGGAACACTCTGAACCTTAATCATACAAGTGTATG  
 AATGACGCAGTGCTCTGAGGAAAGGTTAATAGAACCTTGACAGTACCTGGATAAAGACCACTATACCTGATTG  
 ATCAATCTCCAGTAGCAGCCATCTTGCCAAAGAAAGTAAATTTGATGAAGTCTATGAAGCACTAACTCAGCGT  
 CATCCTAATCTTACTGTTTACAAAAGAAAGACGTTCCAGAAAGGTGGCATTACAAATACAACAGTCCAATTTCA  
 ACCAATCATAGCAGTGGCTGATGAAGGGTGGCACAATTTACAGAATAAGTCAGATGACTTCTGTTAGGCAACC  
 ACGGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTTAGCCCATGGTCTGCTTCTCTATTGGGAAGAAATTC  
 TCAAAAGAGCCATGAATCCACAGATTTGTACCACTACTATGCCACCTCCTCAATATCACTGCCATGCCACA  
 CAATGGATCATTTCTGGAATGTCCAGGATCTGCTCAATTGACCAATGCCAAGGGTGGTCCCTTATACACAGAGTA  
 CTATACTCCTCCTCGGTAGTGTAAACCAGCAGAATATGACCAAGAGGGGTATACCCCTATTTTATAGGGGTG  
 TCTCTTGGCAGCATTTATAGTGATTGATTTTTTTGTAATTTTCATTAAAGCATTAAATTCACAGTCAAAATACCTGC  
 CTTACAAGATATGCATGCTGAAATAGCTCAACCATTATTACAAGCCTTAATGTTACTTTGAAGTGGATTGTCATA  
 TTGAAGTGGAGATTCCATAATATATGTCAGTGTTTAAAGGTTTCAAATTCGGGGAACCGAGTTCCAAACATCTGC  
 AGAAACCATTAAGCAGTTACATATTTAGGTATACACACACACACACACACACACACACACACACACAGGACCAA  
 ATACTTACACCTGCAAAGGAATAAAGATGTGAGAGTATGTCTCCATTTGTTCACTGTAGCATAGGGATAGATAAG  
 ATCCTGCTTTATTTGGACTTGGCGAGATAATGTATATTTAGCAACTTTGCACTATGTAAAGTACCTTATAT  
 ATTGCACTTTAAATTTCTCTCTGATGGGTACTTTAATTTGAAATGCACCTTTATGGACAGTTATGTCTTATAAC  
 TTGATTGAAATGCAACTTTTTCACCCATGTACAGAACTACTGTTACGCATTGTTCAAACGTGAAGGAAAT  
 TCTAATAATCCGAATAATGAACATAGAAATCTATCTCCATAAATGAGAGAGAAGAGGTGATAAGTGTGGA  
 AAATTAATATGTGAATCCTTTGAACCTTGAATTTGGAGATGATTCCCAACAGCAGAATGCAACTGTGGGCAT  
 TTCTGTCTTATTTCTTCCAGAGAACGTGTTTTTATTATTTTCCCTCAAAGAGAGTCAAATACTGACAG  
 ATTGCTCTAAATATATGTTTCTGTCTATAAAATATTGTGATTTCTGTATGAGTCAATAGTGTGATTTTCA  
 TAATAATGAAGCACCACTGAATATCTTTCTCTATATAGTTTCAGCAATGGCCTGAATAGCAGCAACAGGCA  
 CCATCTCAGCAATGTTTTCTTGTGTTGTAATTTATTTGCTCCTTTGAAATTAATCACTATTAAATACATTA  
 AATCAATTTGGTAAAAAAGGAAAAAAAAA

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**FIGURE 202**

MTSKFILVSVFILAALSLSTTFSLQLDQQKVLVVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK  
QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNXSFSLDHMNIYDSKFWEEATPIW  
ITNQRAUGHTSGAAMWPGTDVKIHKRFPTHYPYNESVSFEDRVAKIVEWFTSKEPINLGLLY  
WEDPDDMGHHLGPDSPLMGPFVISIDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEER  
LIELDQYLDKDHYTELIDQSPVAAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN  
SRIQPIIAVADEGWHLQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD  
LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYQTSTILLPGSVKPAEYDQEGSYPYF  
IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

**Signal Peptide:**

amino acids 1-22

**Transmembrane Domain:**

amino acids 429-452

**N-glycosylation sites:**

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

**Somatomedin B Domain:**

amino acids 69-85

**Sulfatase protein Region:**

amino acids 212-241

**FIGURE 203**

GGATTTTGTGATCCGCGATTGCTCCACGGGCGGGACCTTTGTAAC TGCGGGAGGCCAG  
GACAGGCCACCTGCGGGGCGGGAGGCAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGC  
AGAGAGGCCAAGCCCCCTTGCCTTGGGTACACAGCCAAAGGAGGCAGAGCCAGAATCACAA  
CCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACGAAAAGGCAGTCACCCGAGGGCC  
AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACTTCACGGTCGTGGGAGACGA  
CTACCATGCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGG  
AGCAGCCACCACCCACACCACTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCTGACGTTGCC  
CCTGCCCCTGCCCCGACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTT  
CAGCTCCACAGGTTTCAGGTCATCATCATCTGCTTGGTGGTTCTGGATGCCCTCCTGGTG  
TTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCGACAAGAATAACTATGCTGCCATG  
GTATTCCTACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCTTTAAAT  
ATTTGTCTTCCGCTGAGTTCTTTACCACAAGTTTGAGATCCTGGATGCCGCTCGTGGTGG  
TGGTCTCATTCATCCTGGACATTGTCTCTCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGC  
CTGCTGATTCTGCTCCGCTGTGGCGGGTGGCCCCGGATCATCAATGGGATTATCATCTCAGT  
TAAGACACGTTCAGAACGGCAACTCTTAAGGTTAAAACAGATGAATGTACAATTGGCCGCCA  
AGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCCCTGGACTGATGAGTTTGTGTATC  
AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT  
CACACAGCCACCGTGAAAGTCCTGGAGTAAATGTGCTGTACAGAAGAGAGAGAAGGAAG  
CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTA  
TCACTTCAGATTACAAATCACACAGAGCATCTGCCTGTTTTCAATCACAGAGAACAAAACC  
AAAATCTATAAAGATATTCTGAAAATATGACAGAATTTGACAAATAAAGCATAAACGTGTA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 204**

MATWDEKAVTRRAKVAPAERMASKFLRHFTVVGDDYHAWNINYYKKWENEEEEEEQQPPPTPV  
SGEEGRAAAPDVAPAPGPAPRAPLDFRGMLRKLFSSHRFQVIIICLVVLDALLVLAELILD  
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLLSFTTSLRSWMPVVVVVSFILDI  
VLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLRLKQMNVLAAKIQHLEFS  
CSEKPLD

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**FIGURE 205**

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCGAGTGGAGCACCCAGCAGGCCGCCAACAT  
 GCTCTGTCTGTGCTGTACGTGCCGGTCACTCGGGGAAGCCAGACCGAGTTCAGTACTTTG  
 AGTCGAAGGGGCTCCCTGCCGAGCTGAAGTCCATTTTCAAGCTCAGTGTCTTCATCCCTCC  
 CAGGAATTTCCACCTACCGCCAGTGAAGCAGAAAAATTTGTAACAGCTGGAGATAAGGACCT  
 TGATGGGCAGCTAGACTTTGAAGAATTTGTCATTATCTCCAAGATCATGAGAAGAAGCTGA  
 GGCTGGTGTTTAAAGATTTTGGACAAAAAGATGATGGACGCTATTGACGCCGAGGAGATCATG  
 CAGTCCCTGCGGGGACTTTGGGAGTCAAGATATCTGAACAGCAGGCGAAGAAAAATTTCAAGAG  
 CATGGATAAAAACGCGACCATGACCATCGACTGGAACGAGTGGAGAGACTACCACCTCCTCC  
 ACCCCGTGGAAAAACATCCCGAGATCATCCTCTACTGGAAGCAATGCCAGTCTTTGATGTG  
 GGTGAGAATCTAACGGTCCCGGATGAGTTCACAGTGGAGGAGAGGCAGACGGGGATGTGGTG  
 GAGACACCTGGTGGCAGGAGGTTGGGGCAGGGGCGGTATCCAGAACCCTGCACGGCCCCCTGG  
 ACAGGCTCAAGTGTCTCATGAGAAGGAGGGGCCAGGTCACTCTGGCGGGGCAATGGCATCAA  
 GGCTCTCACTCAGATGATTCGAGAAGGAGGGGCCAGGTCACTCTGGCGGGGCAATGGCATCAA  
 GCTCTCAAAATTTGCCCGAATCAGCCATCAAATTCATGGCCTATGAGCAGATCAAGCGCC  
 TTGTGTGTAGTGACCCAGGAGACTCTGAGGATTCAGGAGGCTTGTGGCAGGGTCCCTTGGCA  
 GGGGCCATCGCCAGAGCAGCATCTACCCAAATGGAGGCTCTGAAGACCCGGATGGCGCTGGG  
 GAAGACAGCCGAGTACTCAGGAATGCTGGACTGCGCCAGGAGGATCTGGCCAGAGAGGGGG  
 TGGCGGCTCTACAAAGGCTATGTCCCCAACATGCTGGGCATCATCCCCATTGCCCGCATC  
 GACTTCGACTCTAGAGCTCTCAGAGCGCTCAAGAATGCTGCTGAGCAGCATTCAGTGAAGCAGC  
 GGACCTCGGGCTGTTTGTGCTCTGGCCTGTGGCACCATTGTCAGTACCTGTGGCCAGCTGG  
 CCAGCTACCCCTGGCCCTAGTCAGGACCCGAGTCTGAGGCGCAAGCCCTCTATTGAGGGCGCT  
 CCGGAGGTGACCATGAGCAGCCCTCTTCAAACATATCCTCGGACCCGAGGGGGCTCTGGGCT  
 GTACAGGGGGCTGGCCCCCAACTTCATGAAGGTTCATCCAGCTGTGAGCATCAGCTAGCTGG  
 TCTACGGAAGCTGAAGATCACCTGGGCGTGCAGTTCGCGGTGAGCGGGGGAGGGGCCGCCG  
 CGAGTGGACTCGCTGATCTTGGGCCGAGCCTGGGGTGTGACGCCATCTATTGTGAATG  
 TGCCAACACTAAGCTCTCTCGAGCCAAGCTGTGAAAACCTAGACAGCACCCGAGGAGGGT  
 GGGGAGAGCTGCGAGGCCAGGCTTGTCTGCTGACCCCGAGCAGCCCTCTTGTGTTCC  
 AGCGAAGAGCTGCGAGGCCATTCCTTAGGCTCAGGGTTCAGAGGCTCGGGCTCAGATGTGTAA  
 GGACAGGACATTTTCTGAGTGCCTGCCAATAGTGAAGTGGAGCCTGGAGGCCGGCTTAGT  
 TCTTCCATTTACCCCTTGACGCCAGCTGTTGGCCACGGCCCCCTGCTCTGTTGTGCCGTG  
 ATCTCCTGTGCTCTTCTGCTGCTGCTGTCTGCTGAGGTAAAGTGGGAGGAGGGCTACAG  
 CACATCCACCCCTCGTCCAATCCCATATCCATGATGAAAGGTGAGGTTCAGTGGCT  
 CCGAGGCTGACTTCCCAACCTACAGCATGACGCCAACTTGGCTGTGAAGGAAGAGGAAG  
 GATCTGGCCTTGTGCTCACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTGGGCATGCT  
 TGGGAGTGCAGGAGGGGCTCGGGCTGCTGGCCTGGCTGCACAGAAGGCAGTGTCTGGGCTCA  
 TGGTCTGAGCTGGCTGGCCAGGCTGTGAGGATGGGCCCACTCAGAACCAACTCACTG  
 TCCCACTGTGGCATGAGGCGAGTGGAGCACCATTGTTGAGGGCGAAGGCGAGCGTTTGT  
 TTGTCTGGGGAGGGAAGGAAGGTTGTTGAGGGCTTAATTTAGGACTGTTGGGAAAAGGG  
 TTTTGTCCAGAAGACAAGCCGACAAATGAGCACTTCTGTGCTTCCAGAGGAGGAGGAGG  
 GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGACGCCCTGGGGTTCCTGTCCAAC  
 CCAGCAGGGGCGAGCGGACCCAGCCACATTCCACTTGTGTCACTGCTTGGATGTGACTTAT  
 ATTTTGTATTTTATTTGAACAGAGTTATGCTCAACTATTTTATAGATTTGTTTAAATTAATA  
 GCTTGTCAATTTTCAAGTTCAATTTTTATTCAATTTATGTTATGTTGATGTGACTTATTT  
 AAGCGCCGCCAGTGGGATGGGAGGAGGAGGAGAAGGGGGGCTTGGGCGCTCGAGTCACT  
 CTGTCCAGAGAAATTCCTTTTGGGACTGGAGCGAAGGCGGCGAGGAGGAGGAGGAGGCTG  
 GCTCCTTTCCCTTTGGCAGTTGGGGAAGGGCTTGGCCCCAGCCTTAGGATTTTCAGGGTTGA  
 CTGGGGGCTGGAGAGAGGGGAGGAACCTCAATAACCTTGAAGTGGAAATCCAGTTATTTCT  
 CTGCGCTCGAGGGTTCTTTTATTTCACTCTTTTCTGAATGTCAAGGCAGTGGGTGGCTCT  
 CACTGTGAATTTTGTGTGGGCGGGGCTGGAGGAGAGGTTGGGCTGGCTCGCTCCCTCC  
 CAGCCTCTGCTGCTCTGCTTAAACATGCGGGCCAACTGGCGACCTCAGGTTGCACTTCC  
 ATTCACCCAGATACCTGATGAGGAATCTCAATAGGATGCAAGATCAATGCAAAAAAT  
 GTTATCATATGAACATACCTGGAGTCTGTCAAAAAGCAAATTAAGAAAGAAATGGACGTAG  
 AAGTTGTCTATTTAAAGCAAGCTTCAATAAAGTTGTTTCAAGCTGAAAAAAGAAAAA  
 AA

**FIGURE 206**

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIQSQEFSTYRQWKQKIVQAGDKD  
LDGQLDFFEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILK  
SMDKNGTMTIDWNEWDRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW  
WRHLVAGGGGAGAVSRTCTAPLDRLKVLQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGI  
NVLKIPESAIAIKFMAYEQIKRLVGSQDQETLRIHERLVAGSLAGAIQSSIYPMEVLKTRMAL  
RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNS  
ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG  
LYRGLAPNFMKVIPAVSISYVYENLKITLGVQSR

**Important features:****Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 284-304, 339-360, 376-394

**Mitochondrial energy transfer proteins signature.**

amino acids 206-215, 300-309

**N-glycosylation site.**

amino acids 129-133, 169-173

**Elongation Factor-hand calcium-binding protein.**

amino acids 54-73, 85-104, 121-140

**FIGURE 207**

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCAT  
GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG  
 CAATTGCACTCATCATTTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTC  
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACCTTTTGAACCTGACATCAA  
 ACTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA  
 AAGAAGGCAAAGATGAGCTGTGCGAGCAGGATGAAATGTTTCAGAGGCCGGACAGCAGTGTTTT  
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGC  
 TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA  
 AAAGTGGAGCCTTCAGCATGCCGGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG  
 CGGTGTGAGGCTCCCCGATGGTTCCCCAGCCCACAGTGGTCTGGGCATCCCAAGTTGACCA  
 GGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACTCTGAGAATGTGACCA  
 TGAAGGTTGTGCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAA  
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAGGCGGAG  
 TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGCTCTCTCTTTCTTGCCATCAGCT  
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAATAATGTGCCTTGGCCACAAAAAG  
 CATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTACCACCAGATATGACCTAG  
 TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAGAGCA  
 AGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAA  
 GACATATTAGAAGTTGGGAAAATAATTCAATGTGAAGTACAGCAAGTGTGTTAAGAGTGATAAG  
 TAAATGCACGTGGAGACAAGTGATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTACCT  
 GGGGAGTGAGAGGACAGGATAGTGATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTG  
 TAATGTTGCTCTGAGGAAGCCCCGGAAGTCTATCCCAACATATCCACATCTTATATTCCA  
 CAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG  
 GCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCT  
 TGCTTCTCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA  
 ACAGAGCAGTCGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAA  
 AA

**FIGURE 208**

MASLGQILFWSIIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI  
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTD  
AGTYKCYIIITSKGGKGNANLEYKTGAFSMPEVNVNDYNASSETLRCEAPRWFPQPTVVWASQVD  
QGANFSEVSNTSFELNSENVTMKVVSVLNVNTINNTYSCMIENDIAKATGDIKVTESEIKRR  
SHLQLLNSKASLCVSSFFAISWALLPLSPYMLK

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**FIGURE 209**

GAATTTGTAGAAGACAGCGCGTTGCC**ATG**GCGGCGTCTCTGGGGCAGGTGTTGGCTCTGGT  
 GCTGGTGGCCGCTCTGTGGGTGGCACGCGCGCTGCTGAAGCGGGCCTCCGCCGGCCTGC  
 AGCGGGTTCATGAGCCGACCTGGGCCAGCAGTTGCTACAGGAGATGAAGACCTCTTCTTG  
 AATACTGAGTACCTGATGCCCCCTTCTCCTCAACCAGTGTGGATCCCTTCTCTATTACCTCAC  
 CTTGGCATCGACAGATCTGACCCTGGCTGTGCCCATCTGTAACCTCTCTGGCTATCATCTTCA  
 CACTGATTGTTGGGAAGGCCCTTGGAGAAGATATTGGTGGAAAACGTAAGTTAGACTACTGC  
 GAGTGCGGGACGCAGCTCTGTGGATCTCGACATACCTGTGTTAGTTCCTTCCAGAACCCAT  
 CTCCCAGAGTGGGTGAGGACACGGCCTTTTCCCATCCTGCCCTTCTCTGCAGCTGTTTT  
 GCTTCCTTGTGGCCATCAGAGTTCCTTCCCTGGACAGTCTGGAGAAAGACAGAGGCTGGG  
 GTTGGGAT**TGA**AGACCAGACCCCATCTGAGCCCTTCTCCAGCCCTGTACCAGCTCCTACT  
 GGCATGGCTGAGCTCAGACCCTCCTGATTCTGCCTATTATCCAGGAGCAGTTGCTGGCAT  
 GGTGCTACCGTGATAGGAATTTCACTCTGCATCACAGCTCAGTGAGTAAGACCCAGGGGC  
 AACAGTCTACCTTTGAGTGGGCCGAACCCACTTCCAGCTCTGCTGCCTCCAGGAAGCCCCT  
 GGGCCATGAAGTGCTGGCAGTGAGCGGATGGACCTAGCACTCCCTCTCTGGCCTTAGCTT  
 CCTCCTCTCTATGGGGATAACAGCTACCTCATGGATCACATAAGAGAACAAAGGTGAAAG  
 AGTTTGTAACTTCAAGTGCTGTTCAAGTGCAGCTGCGGGGATTAGCACAGGAGACTCTACGCTCA  
 CCTCAGCAACCTTTCTGCCCCAGCAGCTCTCTTCTGCTAACATCTCAGGCTCCAGCCCA  
 GCCACCATTACTGTGGCTGATCTGGACTATCATGGTGGCAGGTTCCATGGACTGCAGAAT  
 CCAGCTCAGTGGAAGGGCCAGCTGCAGACTTTGAGCCAGAAATGCAACGGGAGGCCTCTG  
 GGACTCAGTCAGAGCGCTTTGGCTGAATGAGGGGTGGAACCGAGGGAAGAAGGTGCGTCGGA  
 GTGGCAGATGCAGGAAATGAGCTGTCTATTAGCCTTGCTGCCCCACCCATGAGGTAGGCAG  
 AAATCCTCACTGCCAGCCCCCTCTTAAACAGGTAGAGAGCTGTGAGCCCCAGCCCCACCTGAC  
 TCCAGCACACCTGGCGAGTAGTAGCTGTCAATAAATCTATGTAAACAGACAAAAAAAAAAAA  
 AA

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**FIGURE 210**

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPF  
LNQCGSLLYYLTLASTDLTAVPICNSLAIFTLIVGKALGEDIGGKRKLDYCECGTQLCGS  
RHTCVSSFPEPISPEWVRTRPFPILPFPLQLFCFLVAIRVPFPWTVVRKTEAGVWD

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**FIGURE 211**

CTTCTGTAGGACAGTCCACGAGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG  
GAAGATGACAGCAATTATAGCAGGACCCCTGCCAGGCTGTGCGAAAAGATTCCGCAATAAACT  
TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT  
TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCATGAAGGGCATCCTCG  
TTGCTGGTATCACTGCAGTGCTTGTTCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT  
TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG  
CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT  
TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCT  
GCTGAAGAACAACCTTTTCAATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG  
CGATGCCCTGGACCCCTCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTATG  
AATCTAATGGAACCTCCTGTCTGGGAAGCCCTGGAAATGCTATGAAGAAGAACAGTGTGTC  
TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTT  
CAACGTCACTAACGCCACCTGTCTAGTTTCTGTCTGGTGAAAACAAGACTCTTGAGGAGTCA  
TCTTTCGAAAGTTTGAGTGTGCAAAATGTAAACAGCTTAACCCCCACGTCTGCACCAACCACT  
TCCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGCCCTTGCCAGCCTCCTTCTCG  
GGGACTGCTGCCCTGAGGTCTGGGGCTGCACCTTGCCAGCACCCCATTTCTGCTTCTCTG  
AGGTCCAGAGCACCCCTGCGGTGCTGACACCTCTTTCCCTGCTGCCCCGTTTAACTGC  
CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCCTGTCTTCTTATTATTA  
AAGCACTGGTTTCACTGCTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 212**

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSSASSSLET PVR  
LYQNMFCSAENCSEETHITAFTHVHSAEEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAE  
CPACYESNGTSCRGKPWKCYEEEQCVFLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENK  
TLGGVIFRKFEKANVNSLTPTSAPTTSHNVGSKASLYLLALASLLLRLGLLP

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**FIGURE 213**

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGCGAAGGTAGGAGGCA  
 GGGCTTGGCTTCACTGGCCACCTCCCAACCCCAAGAGCCCAGCCCCATGGTCCCCGCGCCG  
 GCGCGTGTGTGGGTCTGCTGCTGAATCTGGGTCCCCGGGCGCGGGGGCCCAAGGCCGTG  
 ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCCATGACCCGCGAG  
 CTACCGGAGCACCGCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA  
 ATGATGCCATGGCCGACGCCACCGCTGGTGGACCAGCGGCTGCCGAGCTCTTGGCCGCC  
 ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGA  
 GGGGGTTGTGATTAATGCCGGAAAGGATAGCACCAGCAGAGAGCTTCCAGTGCGACTCCCA  
 ATACAGCGGGGAGTTCCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG  
 ACTTCAAGCCTGCCGCGTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC  
 CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTCAACCTCACCCACAG  
 CCATGCCATCTCCTGAGGATCTGCGGCTGGTGTGATGCCCTGGGGCCCGTGGCACTGCCAC  
 TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTTCCGGGCGCCT  
 TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAAAGCCTTGACCTATCAACAATGTC  
 CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT  
 GCCTCTCAGAGCACCACAGTACCAGGACCACCACTACCCCTTCCCACCATCCACCTCAG  
 AAGCAGTCCCAGCCTGCCACCCGCCAGCCCCCTGCCAGCCCTGGCTTTTTTGAAACGGGTCA  
 GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA  
 GACAGAAACCAGAGGTAATGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT  
 CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTTAGTACAGAAAAACAAACTGGAAAA  
 CACAA

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**FIGURE 214**

MVPAAGALLWVLLNLGPRAAGAQGLTQTPTEMQRVSLRFGGPMTRSYRSTARTGLPRKTRI  
ILEDENDAMADADRLAGPAAELLAATVSTGFSSRSAINEEDEDGSSEEGVVINAGKDSTSREL  
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP  
SPSPTAMPSPEDLRLVLPWGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC  
TYQQCPNRLREECPLDTSLCDTNCASQSTTSTRTTTTPFPTIHLRSSPSLPPASPCPALA  
FWKRVRIGLEDIWNSLSSVFTEMQPIDRNQR

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**FIGURE 215**

CCCGGGTCGACCCAGCGTCCGGGGAGAAAGG**ATG**SCCGGCTGGCGGCGGGTTGGTCTGCTAGCTGGGGCA  
 GCGGCGCTGGCGAGCGGCTCCAGGGCGACCGTGACCGGCTGTACCGCGACTCGGTACTCAGTGGCAGAGCA  
 GAACCTGCTCTGGGGCGCTCTGAATCACTTCGCTCCCGCCAGCAATACATAGTCTTAGCAGGCTGGACCT  
 GTCGGGACGACTGTAAGTATGACTGTATGTGGGTCAACGCTTGGGCTCTACCTCCAGGAAGGTCAAAAGTGGCT  
 CAGTTCCATGGCAAGTGGCCCTTCGCCGTTCTGTTCTTCAAGAGCCGGCATCGGCGCTGGCTCGTTTCT  
 CAATGGGCTGGCCAGCTGGTGATGCTCTGCGCTACCGCACCTTCGTGCCAGGCTCTCCCCATGTACACCA  
 CCTGTGGGCTTCGCTGGGTGCCCTCAATGCATGGTTCTGGTCCACAGTCTTCCACACAGGACACTGAC  
 CTCACAGAGAAATGGACTACTTCTGTGCCTCCACTGTATCCTACACTCAATCTACCTGTGCTCGCTCAGGAC  
 CGTGGGCTGACGACCCAGCTGTGGTCAGTGCTTCCGGGCTCTCCTGCTGCTCATGCTGACCGTGACGCTCT  
 CCTACCTGAGCCTCATCCGCTCGACTATGGCTACAACCTGGTGGCCAACTGGGCTATTGGCCTGGTCAACGTG  
 GTGTGGTGGCTGGCTGGTGGCTGTGGAAACAGCGGCGGCTGCTCAGGTGCGCAAGTGGCTGGTGGTGGTCTT  
 GCTGCTGCGAGGGGCTGTCCTGCTCGAGCTGCTTGACTTCCCAACGCTCTTCTGGGCTCTGGATGCCCATGCCA  
 TCTGGCACATCAGCACCATCCCTGTCCAGCTCCTCTTTTTCAGCTTCTGGAAGATGACAGCCTGTACCTGCTG  
 AAGGAATCAGAGGACAAGTTCAAGCTGGAG**TGA**AGACCTTGGAGCGAGTCTGCCCGAGTGGGGATCCTGCCCGC  
 GCCCTGCTGGCTCCCTTCTCCCTCAACCTTGAGATGATTTCTCTTTTCAACTTCTGAACTTGGACATGA  
 AGGATGTGGGCCAGAAATCATGTGGCCAGCCACCCCTGTGGGCCCTCACCAGCCTTGGAGTCTGTTCTAGGG  
 AAGGCTCCCGACATCTGGGACTCGAGAGTGGGCGCCCTCTACCTCCTGGAGCTGAACTGGGGTGGAACTGA  
 GTGTGTTCTTAGCTCTACCGGGAGGACAGCTGCCCTGTTTCTCCCAACAGCCTCTCTCCACATCCCGAGCTG  
 CCTGGCTGGTCTGAAGCCTCTGTCTAOCCTGGGAGACAGGAGACCAAGGCTTAGGGATACAGGGGGTCCC  
 CTCTGTATACACCCCGCCACCTCTCCAGGACACCACTAGGTGGTGTGGATGCTGTTCTTTGGCCAGCCAA  
 GGTTCACGGCGATCTCCCATGGATCTTAGGGACCAAGCTGTGGGATGGGAAGGAGTTTCAACCTGACC  
 GTTCCCTAGCCAGGTTCACAGGAGCCTCACCATACTCCCTTCAGGGCCAGGGCTCCAGCAAGCCCGAGGCA  
 AGGATCCTGTGCTGCTGTCTGGTTGAGAGCCTGCCACGCTGTGTCGGAGTGGGGCCAGGCTGAGTGCATAGG  
 TGACAGGCGTACGACATGGGCTGGGTGTGTGTGAGCTCAGGCTAGGTGGCAGTGTGGAGACGGGTGTGT  
 CGGGGAAGAGCTGTGGCTCAAAGTGTGTGTGTGCAAGGGGTGGGTGTGTAGCGTGGGTAGGGGAACGTGTG  
 TGCGCGTGTGCTGGCATGTAGATGAGTGACTGCCGCTGAATGTGTCCACAGTTGAGAGGTGGAGCAGGAT  
 GAGGGAATCCTGTACCATCAATAATCACTTCTGGAGGCCAGCTCTGCCCAAGACGCCACCTTGGCGGACAGC  
 CAGGAGCTCTCCATGGCCAGGCTGCCCTGTGTGCATGTTCCTGTGCTGGTGGCCCTTGGCCGCTCTTGCAAC  
 CTCACAGGCTCCCCACACAACAGTGCCTCCAGAAAGCCGCTCCGAGGACAGGAAGGAAATGGGATGGC  
 TGGGGCTCTCTCCATCCTCCTTTCTCCTTGCCCTGCCATGGCTGGCCTTCCCTCCTCAAAACCTCCATCCCT  
 GCTGCCAGCCCTTTGCCATAGCTGATTTTGGGGAGGAGGAAGGGCGGATTGAGGAGCAAGGGGAGAAAGT  
 TATGGCTGGGTCTGGTTTCTTCCCTCCAGAGGGTCTTACTGTTCCAGGGTGGCCAGGGCAGGACAGGGCC  
 ACATATGCTGTGCCCTGGTAAAGGTGACCCCTGCCATTTACAGCAGCCTTGGCATGTTCTGCCCCACAG  
 AATAGAATGGAGGGAGCTCCAGAACTTTCATCCCAAAAGGCAGTCTCGGTGGTTGAAGCAGACTGGATTTTTC  
 CTCTGCCCTGACCCCTTGTCCCTCTTTGAGGGAGGGAGCTATGCTAGGACTCCAACCTCAGGAGCTCGGGT  
 GCCTGCGCTAGCTCTTTTGATACTGAAACTTTAAGGTGGGAGGTGGCAGGGATGTGCTTAATAAATCAA  
 TTCCAAGCCTCAAAAAAAAAAAAAAAAAA

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**FIGURE 216**

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW  
TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWFFSRFLFFQEPASAVASFLNGLASLVMLCR  
YRTFVPASSPMYHTCVAFAWVSLNAFWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR  
TVGLQHPAVVSAFRALLLLMLTVHVSYLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR  
RLPHVRKCVVVVLLQLGLSLELLLDFFPLFWVLDAAHAIWHISTIPVHVLFFSFLEDDSLYLL  
KESDKFKLD

**Important features:****Signal peptide:**

amino acids 1-20

**Transmembrane domains:**

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

**N-glycosylation site.**

amino acids 40-44

**N-myristoylation site.**

amino acids 43-49

**CUB domain proteins profile.**

amino acids 285-302

**Amiloride-sensitive sodium channels proteins.**

amino acids 162-186

0099067-240660



**FIGURE 217**

GGCCGCTGGAATGTGGGAGTTGTGTCTGCCACTCGGCTGCCGGAGGCCGAAGGTCCGTGA  
 CTATGGCTCCCCAGAGCCTGCCTTCATCTAGGATGGCTCCTCTGGGCATGCTGCTTGGGCTG  
 CTGATGGCCGCTGCTTCACCTTCTGCCTCAGTCATCAGAACCTGAAGGAGTTGCCCTGAC  
 CAACCCAGAGAAGAGCAGCACCAAAGAAACGGAGAGAAAAGAAACCAAGCCGAGGAGGAGC  
 TGGATGCCGAAGTCTTGAGGTGTTCCACCCGACGCATGAGTGGCAGGCCCTTCAGCCAGGG  
 CAGGCTGTCCCTGCAGGATCCCACGTACGGCTGAATCTTCAGACTGGGGAAAGAGAGGCCAAA  
 ACTCCAATATGAGGACAAGTTCGAAATAATTTGAAAGGCAAAAGGCTGGATATCAACACCA  
 ACACCTACACATCTCAGGATCTCAAGAGTGCCTGGCAAATTCAGGAGGGGGCAGAGATG  
 GAGAGTTCAAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAAGCGGCTCTTCCGCCCCATTGA  
 GGAACGAAGAAAGACTTTGATGAGCTGAATGTTGTCTATTGAGACTGACATGCAGATCATGG  
 TACGGCTGATCAACAAGTTCAATAGTTCCAGCTCCAGTTTGAAGAGAAGATTGCTGCGCTC  
 TTTGATCTTGAATATTATGTCCATCAGATGGACAATGCGCAGGACCTGCTTTCCTTTGGTGG  
 TCTTCAAGTGGTGATCAATGGGCTGAACAGCACAGAGCCCCCTCGTGAAGGAGTATGCTGCGT  
 TTGTGCTGGGCGCTGCGCTTTTCCAGCAACCCCAAGGTCCAGGTGGAGGCCATCGAAGGGGA  
 GCCCTGCAGAAGCTGCTGGTCATCTTGGCCACGGAGCAGCCGCTCACTGCAAAGAAGAAGGT  
 CCTGTTTGCCTGTGCTCCCTGCTGCGCCACTTCCCCTATGCCAGCGGCAGTTCCCTGAAGC  
 TCGGGGGGCTGCAGGTCTGAGGACCTGGTGCAGGAGAAGGGCACGGAGGTGCTCGCCGTG  
 CGCTGGTCACACTGCTCTACGACCTGGTCACGGAGAAGATGTTGCGCCGAGGAGGAGGCTGA  
 GCTGACCCAGGAGATGTCCCCAGAGAAGCTGCAGCAGTATCGCCAGGTACACCTCCTGCCAG  
 GCCTGTGGGAACAGGGCTGGTGCAGATCACGGCCACCTCCTGGCGCTGCCCGAGCATGAT  
 GCCCGTGAGAAGGTGCTGCAGACACTGGGCGTCTCCTGACCACCTGCCGGGACCGTACCG  
 TCAGGACCCCCAGCTCGGCAGGACACTGGCCAGCCTGCAGGCTGAGTACCAGGTGCTGGCCA  
 GCCTGGAGCTGCAGGATGGTGAGGACGAGGGCTACTTCCAGGAGCTGCTGGGCTCTGTCAAC  
 AGCTTGCTGAAGGAGCTGAGATGAAGGCCCCACACCAGGACTGGACTGGGATGCCGCTAGTGA  
 GGCTGAGGGGTGCCAGCTGGGTGGGCTTCTCAGGCAGGAGGACATCTTGGCAGTGCTGGCT  
 TGCCATTAAATGGAACCTGAAGGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AA

**FIGURE 218**

MAPQSLPSSRMAPLGMMLGLLMAACFTFCLSHQNLKEFALTNPESSTKETERKETKAEEL  
 DAEVLEVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN  
 TTTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV  
 RLINKFNSSSSSLEEKIAALFDLEYVYVHQM DNAQDLLSFGGLQVINGLNSTEPLVKEYAFA  
 VLGAAFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL  
 GGLQVLRITLVQEKGTEVLAVRVVTTLLYDLVTEKMFEEEEAELTQEMSPEKLQQYRQVHLLPG  
 LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDYRQDPQLGRTLASLQAEYQVLAS  
 LELQDGEDEGYFQELLGSVNSLLKELR

**Important features:****Signal peptide:**

amino acids 1-29

**Hypothetical YJL126w/YLR351c/yhcX family protein.**

amino acids 364-373

**N-glycosylation site.**

amino acids 193-197, 236-240

**N-myristoylation site.**

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

**Homologous region SLS1 protein.**

amino acids 68-340

0990437.11601  
109911/240660

**FIGURE 219**

TTCGGCTTCCGTAGAGGAAGTGGCGGGACCTTCATTGGGGTTCGGTTCCCCCCTTCCC  
 CTCCCCGGGGTCTGGGGGTGACATTGCACCGCGCCCTCGTGGGGTCGCGTTGCCACCCCA  
 CGCGGACTCCCCAGCTGGCGGGCCCTCCCATTTGCCGTGTCTGGTCAAGGCCCCACCCCC  
 TTCCCACCTGACCAGCC**ATG**GGGGGTGCGGTGTTTTTCGGGTGCACTTTTCGTGCGGTTGCGG  
 CCGGCTTTCGCGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCTGGT  
 CGCAGGGGCATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCCTCTGTGGTCTGGTTTATCTTGG  
 TCCATGTGACCGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCT  
 GTCTCTGTCTTCTACAGGAGGTGTCCGCTTTGCCCTACTACAAGCTGCTTAAGAAGGCAGA  
 TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCT  
 ATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCT  
 GATGCACTTTGGGCGAGGTGTGGTTGGGATCCATGGGAGCTCACCCATTACTTCTGACTTC  
 AGCCTTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATG  
 CCTGTGAGAGGAGACGGTACTGGGCTTTGGGCTTGGTGGTTGGGAGTCACCTACTGACATCG  
 GGACTGACATTCCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCCATCTATGCAGTCACTGT  
 TTCCATGGGGCTCTGGGCTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTACAGCGAGCC  
 TCTTGTTGTAAGGAC**TGA**CTACCTGGACTGATCGCTGACAGATCCACCTGCCTGTCCACTG  
 CCCATGACTGAGCCAGCCAGCCAGCCGGGTCCATTGCCACATTTCTGTCTCCTTCTCGTC  
 GGTCTACCCCACTACCTCCAGGGTTTTGCTTTGTCTTTTGTGACCCGTTAGTCTCTAAGCTT  
 TACCAGGAGCAGCTGGGTTCAGCCAGTCACTGACTGGTGGGTTTGAATCTGCACTTATCCC  
 CACCACCTGGGGACCCCTTGTGTGTCCAGGACTCCCGCTGTGTGCTGCTGCTCTCAC  
 CCTGCCCAAGACTCACCTCCCTTCCCTCTGCGAGCCGACGGCAGGAGGACAGTCGGGTGAT  
 GGTGTATTCGCGCTCGGCATCCACCCGAGGACTGAGGGAACTAGGGGGGACCCCTGGGC  
 CTGGGGTGCCCTCCTGATGTCTCGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGCA  
 GTTGCCAAGAAAAGGGACCTAGTTTAGCCATTGCCCTGGAGATGAAATTAATGGAGGCTCAA  
 GGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTTCTC  
 AGGCCTGAGGGGGAACCATTTTTGGTGTGATAAATACCCATAAAGTGCCTTTTTTCTTTTTT  
 GAGGTGGGGGGAGGGAGGAGGTATATGGAACCTCTTAACCTCCTTGGGCTATATTTTCTC  
 TCCTCGAGTTGCTCTCATGGCTGGGCTCATTTTCGGTCCCTTTCTCCTTGGTCCAGACCTT  
 GGGGGAAGGAAGGAAGTGCATGTTTGGGAACCTGGCATTACTGGAATAATGGTTTAAACCT  
 CCTTAACCCAGCATCCCTCCTCTCCCCAAGGTGAAGTGGAGGGTGCTGTGGTGAGCTGCG  
 CACTCCAGAGCTGCAGTGCCACTGGAGGAGTCAAGTACCATGACATCGTAGGGAAGGAGGG  
 GAGATTTTTTGTAGTTTTTAATGGGGGTGTGGGAGGGGGGGGAGGTTTTCTATAAACTGT  
 ATCATTTTCTGCTAGGGTGGAGTGTCCATCCTTTTAATCAAGGTGATTGTGATTTTGAAT  
 AATAAAAAAGATTTGTAAAAA  
 AA

0996437.11501

MGAAVF~~FGCTF~~VAFGPAFALFLITVAGDPLRVIILVAGAFFWLVSLLLASVWVFILVHVTDR  
SDARLQYGLLI~~FGAA~~SVLLQEVFRFAYYKLLKKADEGLASLSE~~DGR~~SPISIRQMAYVSGLS  
FGIISGVFSVINILADALGPGVVGIHGDSPPYFLTSAFLTAAIILLT~~FWG~~VVFFDACERR  
Y~~WAL~~GLVVGSHLLTSGTLFNLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQ~~RS~~LLCKD

**FIGURE 221**

AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTGTTGAGTGAGGACGGAAGATCAACCCA  
TTTCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT  
TNTCTGTTATCAATATTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC  
TCACCTATTANTTCCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

0990437.11501

**FIGURE 222**

GACCGACCGTTCAGATGCCCCGGTTCCAGTACGGCTTCCTGATTTTGGTGCTGCTGTNTCTG  
TCCTTCTACAGGAGGTGTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG  
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTCCATCCGCCAGATGGCCTATGTTTN  
TGGTNTTTCCTTCGGTATCATCAGTGGTGTNTTNTCTGTTATCAATATTTGGNTGATGCAN  
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCCCTATTAATTCCTGAATTCAGCCTTT  
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTGTATGCCTGTGA  
GAGGAG

0090437.11501

NGTTGGAGAAAGTGGCGGGACANTTCATTGGGGTTTCGGTTTCCCCCTTTCCTTCCCCG  
GGGTCTGGGGTGACATTGCACGGGCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC  
CCAGNTGGNGCGCCCTTCCCATTTGCCTGTCCTGGTCAGGCCCCACCCCTTCCCAANTG  
ACCAGCCATGGGGGCTCGGGTGTTTTTTCGGCTGCACTTTCGTGCGTTTCGGCCCGGCCTTCG  
CGCTTTTCTTGATCACGTGGCTGGGGACCCGCTTCGCGTTATCATCTGTGTCGAGGGCA  
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTATCTTGGTCCATGTGAC  
CGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGTCTGTCTCTGTTC  
TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA  
GCATCGCTGAGTGAGGACGGAAGATACCCATCTCCATCCGCCAGATGGCTATGTTCTTGG  
TCTCTCCTTCGGTATCATGATGCGGTGTCTTCTCTGTATCAATATTTGGCTGATGCACTTG  
GGCCAGGTGTGGTTGGGATCCATGGAGACTACCC

**FIGURE 224**

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCCCCTTCCCNTTCCCCGGGG  
TCTGGGGGTGACATTGCACCGCGCCCNTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC  
CAGNTGGCGCGCCCTCCCATTTGCCTGTCCTGGTCAGGCCCCACCCCCCTTCCCACCTGA  
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACTTTCGTGCGTTTCGGGCCCGGCCTTC  
GCGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGAGGGGC  
ATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTGGTCCATGTGA  
CCGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGCTCTGTG  
CTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGT  
AGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTG  
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACCT  
GGGCCAGGTGTGGTTGGGATCCATGGAGAC



**FIGURE 225**

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCAGAGCCAGGAGGAGGCAG  
 TGGCCAGGAAGGCACAGGCCCTGAGAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC  
 TACCTGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGG  
 TGTCTGTGCGTCTGCACCCACATCTTTCTCTGTCCCTCCTTGCCCTGTCTGGAGGCTGTCT  
 AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT  
 CTTGTGGTTTCTCTCTACCTGGGGAAATAAGGTGCAGCGGCC**ATG**GGCTACAGCAAGACCCC  
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTT  
 CTCGCCAACAATGATGTTTCTGTGACACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA  
 GGACCTGGGAGCTGGGGCCGGGAAGACGCCGGTGGATGACAGCAGCAGCCGCATCATCA  
 ATGGATCCGACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCCAAC  
 CAGCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGGCCGCCCACTGCAG  
 GAAGAAAGTTTTCAGAGTCCGTCTCGGCCACTACTCGCTGTCAACAGTTTATGAATCTGGGC  
 AGCAGATGTTCCAGGGGGTCAAATCCATCCCCACCCCTGGCTACTCCCACCCCTGGCCACTCT  
 AACGACCTCATGCTCATCAAAGTGAACAGAAGAATTCGTCCCACTAAAGATGTCAGACCCAT  
 CAACGCTCTCCTCTCATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAA  
 CCAAGAGCCCCAAGTGCACTTCCCCTAAGGTCTCCAGTGCTGAATATCAGCGTGCTAAGT  
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA  
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC  
 TGCAGGGGACTCGTGTCTGGGGAGATTACCCTTGTGCCCGGCCCAACAGACCGGGTGTCTAC  
 ACGAACCTCTGCAAGTTACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCT**TGA**GTCTAT  
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTCAG  
 ACCCTCATTCCTTCCCAGAGATGTTGAGAATGTTTCATCTCTCCAGCCCTGACCCCATGTCT  
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGTGACCGTGTCTCTAGTTGAACCTGG  
 GAACAATTTCCAAAAGTGTCCAGGGCGGGGGTTCGTCTCAATCTCCCTGGGGCACTTTCAT  
 CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAA  
 CTGAGAAGTGGAATAAAAAA

**FIGURE 226**

MATARPPMMWVLCALITALLGVTEHVLANNVSCDHPSNTVPSGSNQDLGAGAGEDARSDD  
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS  
PVYESGQQMFQGVKSIHPGYSHPGHSNDLMLIKLNRRIPTKDVVRPINVSSHCPSAGTKCL  
VSGWGTTKSPQVHFVKVLQCLNISVLSQKRCEDAYPRQIDDTMFCAGDKAGRDSQCQGDSSGP  
VVCNGSLQGLVSWGDPYCARPNRPGVYTNLCKFTKWIQETIQANS

00000437.11001

**FIGURE 227**

**ATG**GTCAACGACCGGTGGAAGACCATGGGCGGCGCTGCCCAACTTGAGGACCGGCCGCGCGA  
 CAAGCCGACGCGGCCGAGCTGCGGCTACGTGCTGTGCACCGTGTGCTGGCCCTGGCTGTGC  
 TGCTGGCTGAGCTGTCAACGGTGCCGCTGCTTCTGTAACACGCCCCACGCGCCGGGACG  
 GCGCCCCACCTTCTGTCAGCACTGGGGCTGCCAGGCGCAACAGCGCCCTGTGCTACTGTGGA  
 AAGGGCGGACAGCTCGCACCTCAGCATCTCATTTGACCCGCGCTGCCCGACCTCACCGACA  
 GCTTGCACCGCTGGAGAGCGCCAGGCCCTCGGTGCTGCAGGCGCTGCAGAGCAGCAGCGCC  
 CAGCCACGCTGTGTGGCGACAGGAGCAGGAGCTGCTGGACAGCTGGCCGACCAAGCTGCC  
 CCGGCTGCTGGCCCGAGCCCTCAGAGCTGCAGACGGAGTGCATGGGGCTGCGGAAGGGGATG  
 GCACGCTGGGCCAGGGCTCAGCGCCCTGCAGAGTGAGCAGGGCCGCTCATCCAGCTTCTC  
 TCTGAGAGCCAGGGCCACATGGCTCACCTGGTGAACCTCCGTACGCGACATCTGGATGCCCT  
 GCAGAGGACCGGGGGCTGGGCGGCGCCGCAACAAGGCCGACCTTCAGAGAGCGCTGCC  
 GGGGAACCGGCCCGGGGGCTGTGCCACTGGCTCCCGGCCCGGAGACTGTCTGGACGTCTCT  
 CTAAGCGGACAGCAGGAGCATGGCGCTACTCTGTCTTCCACCCACTACCGGGCGGGCT  
 CCAGTGTACTGTGACATGCGCACGGACGGCGCGGCTGGACGGTGTTCAGCGCGGGGAGG  
 ACGGCTCCGTGAACCTTCTCCGGGGCTGGGACGCGTACCGAGACGGCTTTGGCAGGCTCAC  
 GGGGAGCATGGCTAGGGCTCAAGAGGATCCACGCGCTGACCACAGGCTGCCTACGAGCT  
 GCACGTGGACCTGGAGGACTTTGAGATGGCACGGGCTATGCCGCTACGGGAGCTTCGGCG  
 TGGCTTGTGTTCTCCGTGGACCTGAGGAAGACGGGTACCGCTACCGTGGCTGACTATTCC  
 GGCAGCTGAGGCGACTCCCTCCTGAAGCACAGCGGATGAGGTTACGACCAAGGACCGTGA  
 CAGCGACCATTCAGAGAACTGTGCCGCTTCTACCGCGGTGCTGGTGGTACCGCAACT  
 GCCACAGTCCAACCTCAATGGGCGAGTACCTGCGCGGTGCGCACGCTCTATGCCGACGGC  
 GTGGAGTGTCTCTGGACGGGCTGGCAGTACTCAAGTTCTCTGAGATGAAGATCCG  
 CGCGTCCGGGAGGACCGCT**TAG**ACTGGTGCACCTTGCTTGGCCCTGCTGGTCCCTGTGCG  
 CCCATCCCCACCCACCTCACTCTTCTGTAATGTTCTCCACCCACCTGTGCCCTGGCGGAC  
 CCACCTCTCAGTAGGGAGGGGCGGGCCATCCCTGACACGAAGCTCCCTGGGCGGGTGAAGT  
 CACACATCGCTTCTCGCGTCCCGACCCCTCCATTGGCAGCTCACTGATCTCTTGCCTC  
 TGCTGATGGGGCTGGCAACTTGACGACCCCACTCCTGCCTGCCCACTGTGACTCCGG  
 TGCTGTTGGCGTCCCTGGCCAGGATGGTGGAGTCTGCCCGAGGACCCCTGTGCCCTGCC  
 CTAGCAATCGTGGGGAATGTCAAGTCTCTCTGAGGTGAGGTCTGAGGCCAGTATCCTCCAG  
 CCCTCCAATGGCAACCCACCCGTTTCCCTGGTGCCAGAGAACCACCTCTCCCCAA  
 GGGCTCAGCTGGCTTGGGGTGGGTGGCCCATCTACAGGCCCTGAGGTGAGGATGGG  
 GAGCTGCTGCTTTGGGGACCAACGCTCCAAGGCTGAGACAGTTCCCTGGAGGCCACCCAC  
 CCTGTGCCCGGAGGCTGGGGTGTGCAGTCTCTTACCTGCTGTGCCACCTGCTCTCTG  
 TCTCAAATGAGGCCAACCCATCCCCACCCAGCTCCCGGCCCTCTCCTAGGGGAGC  
 CGGGCTGCCATCCATTCTCTGCTCTGGAAGGTGGGTGGGGCCCTGCACCGTGGGGCT  
 GAGCTGCGCTAATGGGAAGCTCTTGGTTTTCTGGGCTGGGGCTAGGCAAGGCTGGGATGAG  
 GCTTTGACAAACCCCAACCAATTTCCAGGGACTCCAGGGTCTGAGGCTCCCAAGGAGG  
 GCTTGGGGGTGATGACCCCTTCCCTGAGGTGGCTGTCTCATGAGGAGGCCAACCCCTGCC  
 ATTGACCGTGGCCACCTGGACCCAGGCCAGGCCCGGCCCGCGAGTGTTCAAGGGACAGGA  
 CCACCTACCGGGCAATTGGGGTGGGGGACTGGGGCACAGACAGGACCAACCTGGACA  
 CTTTCTTGTGTAATCTCCCAACACCCAGCACGCTGTCTATCCCACTCTCTGTGTGCACACA  
 CTTAGAGGTGAGACCCGAGGCTCCAGGACAGCAGCCACAAGGGCAGGGCTGGAGCCGGG  
 TCTCTAGCTGTCTGCTCAGCAGCCCTGGACCCGCGTGCCTTACGCTCAGGCCAGATCAGAGG  
 CGGCTTTTCCAAGGCTCCTGATGGGGGCTCCGAAAGGGCTGGATCAGCTTGGGGAGCT  
 GCTAGCAGGCTCTCTCTGGGAGGAGGGAGGTGGCTTCTCTCAAAGGACACCCGATGGA  
 GTGCTCAGGGGTGTGGGGTTCCGTTTCCCTTCCCTCCCACTGAAGTTTGTGCTTAA  
 AACAATAAATTTGACTTGGCACCACTGGGGGTGGTGGGAGAGGCGGTGTGACCTGGCTCTC  
 GTGCCAGTGCCACAGCTCATCCACATGCGCAG

**FIGURE 228**

MVNDRWKTMGGAAQLEDPRPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT  
APPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA  
QPRLVGDQEQELDLTLADQLPRLLARASELQTECMGLRKHGHTLGQGLSALQSEQGRLIQLL  
SESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCLDVL  
LSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRRREDGSVNFFRGWDAYRDGFGRLT  
GEHWLGLKRIHALTTQAAAYELHVDLED FENG TAYARYGSFGVGLFSVDPEEDGYPLTVADYS  
GTAGDSLKKHSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASADG  
VEWSSWTGWQYSLKFSEMKIRPVREDR

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**FIGURE 229**

GCAGTCAGAGACTTCCCCTGCCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCT  
 TGCTTCTCTGAAGTACAGTCACAGTAGCCCGCGGCCAGGGCAATCCGACCACATTTCACTCT  
 CACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG  
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC  
 CGCGGCACAGAGCACAGGGCTCCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCCTGCTGAC  
 TTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACC  
 AGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATACGTCC  
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGC  
 TGAAAAACTCTGTCTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG  
 AACAAATGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAG  
 GACTGTAATATTCTGCCTTAGTGAAAACCTCTACCATGCTGAAGATAAACAAACAAGAAGA  
 CCTGGAAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTT  
 TCGCCCTTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACGTG  
 TTCCATATTATAATAGATGTCAACAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGG  
 GATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGCAGGAA  
 TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGAATCGCC  
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAGCAAGGGCTAGTTGAGACAT  
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTCTCTGTG  
 TTTCTGTTCAGGATCACCAGCATTCTGAGCTTGGGTTTATGACGTATTTAACAGTCACA  
 AGAAGTCTTATTACATGCCACCAACCAACCTCAGAAACCCATAATGTGATCTGCCTTCTTG  
 GCTTAGAGATAACTTTTAGCTCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTCAT  
 GTCTTCCTTACACTTGGTGGAATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAC  
 ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATGGCAGTCACTTCCAGATTGTACC  
 AGCAAATACACAAGGAATCTTTTTGTTGTTTCAGTTCACTACTAGTCCCTTCCCAATCCAT  
 CAGTAAAGACCCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG  
 AATCTCAAATCTCAATGCCTTATAAGCATTCCTTCTGTGTCATTAAAGACTCTGATAATTG  
 TCTCCCCTCCATAGGAATTTCTCCCAGGAAAGAAATATATCCCCTCTCCGTTTCATATCAG  
 AACTACCGTCCCCGATATTCCCCTTCAAGAGATTAAAGACCAGAAAAAGTGAGCCCTTCTCA  
 TCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTCCATTGACCCATATTTATACCTTTTACG  
 GTACTGAAGATTTAATAATAAATGTAATACTGTGAAAAA

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230/330

**FIGURE 230**

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCVL  
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKL  
LYNKAGAHRCSPCTEQWKWHGDNQYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLE  
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPETSELFHIIIDVTSPRSRDCVAILNGMI  
CKELKRCVCERRAGMVKPESLHVPETLGEGD

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**FIGURE 231**

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG  
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG  
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTCAACGTGGCGACCAGTGGCCCTGACCCCTG  
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTTCAGTA  
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA  
CGTCCCAAGAGTTGCAATTTNTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTNTGCAGCAT  
GTGGCTGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACTTTGAAGGAGGGCAA  
AGTNTCCTCATNTACTATACACACCACTTCCC

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**FIGURE 232**

GCGGAGCGCAAGAACCCTGCGCAGCCAGAGCAGCTGCTGGAGGGGAATCAGAGGCGCGGCTC  
 CGGGGATTCCGGCTCGGGCCCGTGGCTCTGCTCTGCGGGGAGGGAGCGGGCCCGCCCGGGG  
 CCCGAGCCCTCCGGATCCGCCCTCCCGCTCCCGCCCTCCGAGACTCTCTTGGCTGCT  
 CTGGGGGTTTCGCGGGGCGGGGACCCGCGGTGCGGGGCGCCATGCGGGGCATCGCTGCTGCTG  
 TCGGTGCTGCGGGCCCGCAGGGCCCGTGGCCGTGGGCATCTCCCTGGGCTTCAACCTGAGCGCT  
 GCTCAGCGTCACTTGGGTGGAGGAGCCGTGCGGGCCAGGCCCGCCCAACCTGGAGACTCTG  
 AGCTGCGCGCGCGCGGCAACACCAACGCGGCGCGCGGGCCCAACTCGGTGACGCCCCGGAGCG  
 GAGCGCGAGAAGCCCGGGGCGGCGCAAGGCGCGGGGAGAATTGGGAGCCCGCGCTCTTGCC  
 CTACCACCTGACAGCCCGGCCAGGCGGCCAAAAAGGCCGTGAGGACCCGCTACATCAGCA  
 CGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGGCGGTGCTGACCTCTCAGACCACGCTGCC  
 ACGCTGGGCGTGGCCGTGAACCGCACGCTGGGGCACCGGCTGGAGCGTGGTGTCTCTGAC  
 GGGCGCAGCGGGCGCGCGGGCCCACTGGCATGGCAGTGGTGACGCTGGGCGAGGAGCGAC  
 CCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCTGGAGCAGCACGGCGACGACTTTGAC  
 TGGTTCTTCTGCTGCTGACACCACTACACCGAGGCGCACGGCTGGCACGCCCTAACTGG  
 CCACCTCAGCCTGGCCCTCCGCGGCCCACTGTACCTGGGCGGGCCCGAGGACTTCTCCTGGCG  
 GAGAGCCCAACCCCGCGCTACTGCCACGGAGGCTTTGGGGTGTCTGCTGCGCGCATGCTG  
 TCTCAACAACCTGCGCCCCACCTGGAAGGCTGCCGCAACGACATCGTCACTGCGCGCCCTGA  
 CGAGTGGCTGGGTGCTGCACTTCTCGATGCCACGGGGTGGGCTGCACTGGTGACACGAGG  
 GGGTGCACTATAGCCATCTGGAGCTGAGCCCTGAGCGTGTGCGTGACCTGTGCACATGTACCAGCTGCACAA  
 GTCCGAAGTGGCCCTGACAGCCCAACCTGTGCGTGACCTGTGCACATGTACCAGCTGCACAA  
 AGCTTTGCGCCGAGCTGACTGGAACGACAGTACCAGGAGATCCAGGAGATTACAGTGGCAGA  
 TCCAGAAATCCAGCACTGCTGCCCTGATGGGAGCCCGGCGAGCTGCTGGCCGCTGGGTATT  
 CCAGCACCATCCCGCCCGGCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTACCGGAGCA  
 GCACGCTTTCTCTGCGCCGATGGCTCACCCCGCTGCCACTGCGTGGGGCTGACCCGGCTG  
 ATGTGGCCGATGTTCTGGGGACAGCTCTAGAGGAGCTGAACCGCCGCTACCAACCCGGCCTTG  
 CGGCTCCAGAAGCAGCAGCTGGTGAATGGTACCGACGCTTTGATCCGGCGCGGGGTATGGA  
 ATACACGCTGGACTTGCAGCTGGAGGCACTGACCCCCAGGGAGGCCGCCGGCCCCCTCACTC  
 GCCGAGTGCAGCTGCTCGGCCGCTGAGCCGCTGAGCAGCTGGCCCATGCAGATGTCTTCGACCT  
 GAGGCCCTCAGTCTCACTGTGCTGCTGCCCTAGCTGCGGCTGAGCGTGAACCTGGCCCTGG  
 CTCTTTGGAGGCCCTTTGCCACTGCAGCACTGGAGCCGTGGTATGCTGCGGCAGCCCTGACCC  
 TGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCTGGCCCATGCAGATGTCTTCGACCT  
 GTCAAGGCCCACTGGCAGAGCTGGAGCGCGCTTTCCCGGTGCCCGGTGCCATGGCTCAG  
 TGTGCGACAGCCGCAACCTCACCACTGCGCCCTCATGGATCACTCTCCAAGAAGCACCCCG  
 TGGACACACTGTTCTGCTGGCGGGCCAGACAGGCTGCTCACGCCCTGACTTCTGTAACCGT  
 TGCCGATGATGACCTCTCCGCTGCGGCTGCGAGGCTTTCTTCCATGCACTTTCCAAGCCTTTCA  
 CCCAGGTGTGGCCCCACCACAAGGGCGTGGGCCCCAGAGCTGGGCCGTGACACTGGCCGCT  
 TTGATCGCCAGGCGAGCCAGCGAGGCTGCTTCTACAACTCCGACTACGTGAGTGGTGGCGTGGG  
 CGCCTGGCGGCGAGCTCAGAACAGAGAGGAGCTGCTGGAGAGCCTGGATGTGTACGAGCT  
 GTTCTCTCACTTCTCCAGTGTGCATGTGCTGCGGGCGGTGGAGCCGGCGCTGCTGACGCT  
 ACCGGCCCCAGCGTGCAGCGCGAGGCTCAGTGAGGACCTGTACCCCGCTGCCCTCAGAGC  
 GTGCTTGAAGGCTCTGGCTCCCGAACCCAGCTGCCATGCTACTTTGAACAGGAGCGAGG  
 CAACAGCACTGACCCCACTGTCCCGTGGGCGTGGCATGGCCACACCCCAACCCACTT  
 CTCCCCCAAAACAGAGCCACTGCCAGCCTCGCTGGGCGAGGCTGGCCGTAGCCAGACCC  
 AAGCTGGCCCACTGGTCCCTCTTGCTGCTGCTGGGTCCCTGGGTCTGGACAGCACTGGG  
 GGACGTGCCCCAGAGCCCACTTCTCATCCAAACCACTTTCCCTGCCCTTACGCTG  
 GCTGATTGGGGCTGTGGCCCTCACGATATTTATGAGTACAGTGTGCTGACGCCAGCCCTGC  
 CTTGGGCGCTGGGGCTGGGCTGTAGAAGAGTTGTGGGGAAGGAGGAGCTGAGGAGGG  
 GCATCTCCCACTTCTCCCTTTTGGACCTGCCGAAGCTCCCTGCCTTTAATAAAGTGGCCA  
 AGTGTGAAAAA



**FIGURE 233**

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPFRGNTNAARRP  
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVRTRYISTELGIRQLLVAVL  
TSQTTLP TLGVAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLE  
QHGD DFDWFFLVPD TTYTEAHGLARLTGHL SLASA AHLYLGRPQDFIGGEPTPGRYCHGGFG  
VLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCLDATGVGCTGDHEGVHYSHLELSPGEP  
VQEGDPHFRSALT AHPVRDPVHMYQLHKAFARAE LERTYQEIQELQWEI QNTSHLAVDGDRA  
AAWPVGI PAPS RPASRF EVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLGTAEELN  
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGRRPLTRRVQLLRPLSRVEI  
LPVPYVTEASRLTVLLPLAAERDLAPGFLEAFATAALEPGDAAAALTLLLLYEPRQAQRVA  
HADVFAPVKAHVAELERRFPGARVPWLSVQTAA PSPLRLMDLLSKKHPLDTLFLLAGPDTVL  
TPDFLNRCRMHAISGWQAFFPMHFQAFHPGVAPPQGGPPPELGRDTGRFDRQAASEACFYNS  
DYVAARGRLAAASEQEEELLES LDVYELFLHFSSLHVLR AVEPALLQRYRAQTCSARLSEDL  
YHRCLQSVLEGLGSRTQLAMLLFEQEQQNST

0990437-11601

**FIGURE 234**

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT  
 TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCTAGTGGAGAAAAGGAGT  
 AGCTATTAGCCAATTTCGGCAGGGCCCGCTTTTGAAGCTTGATTTCCTTTGAAGATGAAAG  
 ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAACTCGGGGCGATTGGCTGGGAA  
 CTGTATCCACCCAAATGTCACCGATTTCCTCCTATGCAGGAAATGAGCAGACCCATCAATAA  
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACCTGGAGGCAAAG  
 AGGGTTGCTCAACGCCCCGCCTCATTTGGAAAACCAAATCAGATCTGGGACCTATATAGCGTG  
 GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT  
 TTCCCGCCCCCTGAGACCTGCAGCACCATCTGTCTATGCGGCTGGGCTGTTTGGTTTGAGC  
 GCTCGCCGCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCGGCCGCCCGCTCCGCTGGGA  
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGAAAGCGGCCCCCAGAAC  
 CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTGTATGAGAAGAACCA  
 GACTCCCATGGTTATGACAAGGACCCCGTTTGGACGCTCTGGAACATGCGACTTGTCTTCTT  
 CTTTGGCGTCTCCATCATCTGGTCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA  
 GGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGGC  
 CTTCCCATCATGGAATCCAATGCTTCGACCCAGCAAGATCCAGCTGCCAGAGGATGAGTGA  
 ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC  
 CTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

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**FIGURE 235**

MAAGLFGLSARRLLAAAATRG LPAARVRWESSFSRTVVAPS AVAGKRPEPTTPWQEDPEPE  
DENLYEKNPD SHGYDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER  
LVKYREANGLPIMESNCFDPSKIQLPEDE

0990137.1.1501

**FIGURE 236**

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGC  
TCCCGGCCGCCGCGCTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCGCT  
GTGGCGGGAAAGCGGCCCCAGAACCGACACACCGTGGCAAGAGGACCCAGAACCCGAGGA  
CGAAAACCTTGATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCCGTTTGGACG  
TCTGGAACATGCGACTTGTCTTCTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC  
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT  
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAACCTGCTTCGACCCAGCA  
AGATCCAG

0990437.111501

GCGCGGGCT**ATG**CCGCTTGTCTGCTCTGCTCTGTTGCTCCTGGGGCCCGCGGCTGGTGCCT  
TGCAGAACCCCCACGCCGACAGCCTCGGGGAGGAACCTGTGATCAACCCCGCTGCCCTCCGGGG  
ACGTAGCCGCCACATTCCAGTTTCCGACAGCGCTGGGATTTCGAGACTTCAGCGGGAAGGAGTG  
TCCCATTACAGGCTCTTTCCAAAGCCCTGGGGCAGCTGTATCTCAAGTATCTCTACGGGCA  
GCTGCACCTGTGATTCACCAAGGCTTTTGGAGAGCCGATACTGGGGGCCACCTCTCTCTGC  
AGGCCCATCAGTGCAGAGCTGTGGGCTGTGGTTCAGAACACATGTGCATGTGTGGATTA  
TCTTGAAGGAGCTCAGTAATGTCTCTCATTGAGGATCTCTCGAGCTCTCTCAACTCATCTGA  
TTCACCAACACAGTCACTCCCACTGCTCTCTTCAAACCCCTGGGCTGGCCAAATGACACTG  
ACCATACTTTTCGCGCTATGCTGTGCTGCGCGGGGAGGTGGTCTGCACCGAAACCTCAC  
CCTTGAAGGAGCTCTTGCCCTGTAGTTTCCAAAGCAGCCCTCTCTGTGCTGCTGAAGGCAGA  
TCTGTTTGCACACAGACTACCATTCCAGGAGCTGCATATCCGCGCTGTTTGCGAAGAAAT  
CACGCTGTACTAGCATCTCTGGGAGCTGAGGCAGACACTGTGAGTTGTATTGTATGCTCTT  
ATCACGGGCGAGGGAAGAAGACATGGTCCCTCTCCGGATGTTCTCCCGAACCTCTCAGGA  
GCCCTGCCCCCTGGCTTTCAGAGAGCCGAGTCTATGTGACATCACCACTACAACCGAGACA  
ACGAGACATTAGAGGTGCACACCCCGCACCATACATATCAGGACGTCATCTTAGGACAT  
CGGAAGACCTATGCCATCTAGCTTGCTTGACACCGCCATGATCAACAATCTCGAAACCT  
CAACATCCAGCTCAAGTGAAGAGACCCCCAGAGAATGAGGCCCCCAGTGCCCTTCTCTGC  
TGTGCCACCGGTACGTGATGGTCTATGGGTCGAGAAGGGGAGCTGAGCACACTGCTGTAC  
AACACCCACCATACCGGGCCCTCCCGGCTGCTGCTGTGACACCGGTACCTGTGATCTGCG  
GCTGTATGTGCACACCTCACCATCTCAACTCCAAGGCGAAGGAGAACCAAGTTACATCC  
ATCACAGCTGCCACGAGCCGCTGCAACACCCCACTCTGGAGATGCTGATTAGCTGCGG  
GCCAATCAGTCAACAGGTTTCCATCCAGTTTGAAGCGGGCGCTGCTGAAGTGGACCGAGTA  
CACGGCAGATCTTAACATGGCTTCTATGTACAGCCATCTGTCTCAGCGCCCTTGTGCCCA  
GCTAGGTAGCAGCAAGCCAGTGGACTGGGAAGAGGACTCCCTCTTCAACAGCCTGTTCCCA  
GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC  
GACACCGGACTCAGCATGCCCTACAACGTGATGCTGCCTCAGTGCAGCTGTGTGGCCGTGT  
GTACAGGCTCCTCTTCACAATCTCTCACCGCAACCTTCCATCTGAGGAGGCCCGCAGGT  
GGCTTGGCCAAGCGGCTGCCAACCTTATCCGGCGCGCGAGGTTGCCCCCACTCT**TG**ATT  
CTTGCCCTTTCAGCAGCTGTCAGCTGCGCTTTTCTCTCTGGGAGGGGAGCCCAAGGCTGTT  
TTCGCCACTTGCTCTCTCAGAGTTGCTTTTGAACCAAGTGCCCTGGACAGGTCAGGGC  
CTACAGCTGTGTTTCTCAGTACAGGAGCCGACGAGCAAAATGTGGCATTTGAATTTGAATTA  
CTTAGAAATTCATTTCTCACTGTAGTGAGCCACTCTATATTGAGGTGCTCAATAGCAAAA  
AGTGGTCGGTGGCTGCTGTATTGGACAGCACAGAAAAGATTTCATCTGCACAGAAAGGTC  
GGCTGGCAGCACTGCCCAAGGTCATGGGGTGTGTCACAGTGTATGTCACGTGTAGTGGA  
TGGAGTTTACTGTTTGTGAATTAATAAACCGCTGTTTCCGTGGAAAAAATAAAAA

**FIGURE 238**

MPLALLVLLLLGPGGWCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY  
RLFPKALGQLISKYSLRELHLSFTQGFWRTYWGPPFLQAPSGAELWVWFQDVTVDVDSWK  
ELSNVLSGIFCASLNFIDSTNTVPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK  
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCARNARCTSSISWELRQTLSVVFDAFITG  
QGKKDWSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGTRKT  
YAIYDLLDTAMINNSRNLNIQLKWKRPPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH  
PYRAFPVLLDTPWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS  
VTKVSIOFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD  
GSNYFVRLYTEPLLVLNLTPTDFSMYPNVICLTCTVVAVCYGSFYNLLTRTFHIEEPRTGGLA  
KRLANLIRRARGVPPL

0000437 11501

**FIGURE 239**

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCCTGGTGG  
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCAGCTGACAACGTACGC  
TGCTTCAAGTCCGATCCTCCCAAGTGTACACAGACCAGGACTGTCTGGGGGAAAGGAAGTG  
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCCTGTGAAGGAACTGGAAGAAGGAGGAA  
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC  
TCCTCCTCTACCAGGTGTCTCAGAAATGATGCTGGGTCCTTTCTACCTCTGGGGGTCACTC  
TCACTTGGCACCTGCCCCTGAGGGTCCTGAGACTTGAATATGGAAGAAGCAATACCCAACC  
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAGAGGGAAGAGTCACAAAAAG  
TCCAGACCCAGGGACGGTACTTCCCTCTCTACCTGGTGCTCCTCCCTAATGCTCATGAAT  
GGACCCCTCATGAATGAAACCAAGTGCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC  
TGCAATGTGTGATCAGCTAGAAGGCACTGTCAGAGAAGAGAACTGGTCCTCACCAGATG  
CTGAATCTGCTGGTGCCTTGATCTTGGAATCCCAAGCTCTAGAACTGTAAGAAATAAATAT  
TTGCTGTTTATAATCCAA

0990437.11504

**FIGURE 240**

MGSSSFLVLMVSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC  
YLHCGFKCVIPVKELEEGGNKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

**Signal sequence:**

amino acids 1-19

**N-myristoylation sites:**

amino acids 23-29, 27-33, 32-38, 102-108

**WAP-type 'four-disulfide core' domain signature:**

amino acids 49-63

00000437 111601  
T09111 2400660



**FIGURE 241**

AAACCTCAGCACTTGCCGGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACTTCTGGCCAGG  
 AAACCTGAGCGGTGAGACTCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCC  
 TCTAGAACCCGACCCACCACCA**ATG**AGGTCCTGCCTGTGGAGATGCAGGCACCTGAGCCAAAGG  
 CGTCCAGTGGTCTTGCTTCTGGCTGTCTGGTCTTCTTCTTCTCGCCTTGCCCTCTTTTA  
 TTAAGGAGCCTCAAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTC  
 CTACAGTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTA  
 TGCAGAGCCAGCGCCAGAGAACAATGCCCTCAACACACAAACCCAGCCCAAGGCCACACCA  
 CCGGAGACAGAGGAAAGGAGGCCAACAGGCACCGCCGGAGGAGCAGGACAAGGTGCCCCAC  
 ACAGCACAGAGGGCAGCATGGAAGAGCCAGAAAAAGAGAAAACCATGGTGAACACACTGTC  
 ACCCAGAGGGCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC  
 AGGACACAAGAGCAGCCCAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGAGC  
 GTGTCAGAGAAGCACCCAGGGCAAGCGGCCAACACAGCCAAGACGCTCATTCCTCAAAAGTCA  
 GCACAGAATGCTGGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA  
 CAGCAGTCATCCCACTAAGGAGAAGAAACCTCAGGCCACCCACCCCTGCCCCCTTTCCAG  
 AGCCCCACGACGACAGAAACCAAGACTGAAGGCCGCCAACTTCAAACTGAGCCTCGGTG  
 GGATTTTGAGGAAAAATACAGCTTCGAAATAGGAGGGCTTCAGACGACTTGCCCTGACTCTG  
 TGAAGATCAAAGCCTCCAAGTCGCTGTGGCTCCAGAACTCTTCTGCCCAACCTCACTCTC  
 TTCTGGACTCCAGACACTTCAACCAGAGTGAGTGGGACCGCCTGGAACACTTTGCACCACC  
 CTTTGGCTTCATGGAGCTCAACTACTCCTTGGTGCGAAGGTCGTGACACGCTTCCCTCCAG  
 TGCCCCAGCAGCAGCTGCTCCTGGCCAGCCTCCCGCTGGGAGCCTCCGGTGCACTACCTGT  
 GCCGTGGTGGCAACCGGGGCATCCTGAACAACCTCCACATGGGCCAGGAGATAGACAGTCA  
 CGACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAAGGCTACGAACAGGATGTGGGGACTC  
 GGACATCCTTCTACGGCTTTACCGCCTTCTCCCTGACCCAGTCACTCCTTATATTGGGCAAT  
 CGGGGTTTCAAGAACGTGCCTCTTGGGAAGGACGTCCGCTACTTGCACTTCTCTGGAAGGCAC  
 CCGGGACTATGATGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTT  
 TCTGGTTCAAGGCAGAGCCCCAGGAAGCTTTTTCGGGAAGCCCTGCACATGGACAGGTACCTG  
 TTGCTGCACCCAGACTTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCTGGGA  
 TGGTGCCCACTGGAGGATATACCGCCCCACCACTGGGGCCCTCCTGCTGCTCACTGCCCTTC  
 AGCTCTGTGACCAGGTGAGTGCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT  
 CACTACTATGATACATCATGGAAGCGGCTGATCTTTTACATAAACCATGACTTCAAGCTGGA  
 GAGAGAAGTCTGGAAGCGGCTACACGATGAAGGATAATCCGGCTGTACCCAGGCTCCTGGTC  
 CGGAACTGCCAAAGCCAAAGAAC**TGA**CCGGGGCCAGGGCTGCCATGGTCTCCTTGCCTGCTC  
 CAAGGCACAGACTACAGTGGGAATCTTGAGACTCTTTGGCCATTTCCTATGGCTCAGACTAA  
 GCTCCAGCCCTTCCAGAGTTCGAAGGGAACACTTGAACCATGGACAAGACTCTCTCAAGAT  
 GGCAAATGGCTAATTGAGGTTCTGAAGTTCCTCAGTACATTGCTGTAGGTCCTGAGGCCAGG  
 GATTTTAAATTAATGGGGTGATGGGTGGCCAAATACCAAACTTCTGCTGAAAAACACTCTT  
 CCAGTCCAAAGCTTCTTGATACAGAAAAAGAGCCTGGATTACAGAAACATATAGACTCTG  
 GTTTGAATCCAGATCGAGTTTACAGTTGTGAATCTTGAAGGTATTACTTAACTCACTAC  
 AGATTGTCTAGAAGACCTTTCTAGGAGTTATCTGATTCTAGAAGGGTCTACTCTGTCCCTTG  
 TCTTTAAGCTATTTGACAACCTCACTGTGTGTAGAAAACCTGATAATAATACAAATGATTGTT  
 GTCCATGGAAGGCAATAAATTTTCTACAGTGAIAAAAAAAAAAAAAA

**FIGURE 242**

MRSCLWRCRHLSSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHRQRTENIKERSLQSLAKP  
 KSQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW  
 KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQGNNGQTRKLTASRTVSEKHQG  
 KAATTAKTLIPKSHRMLAPTGAVSTRTRQKGVTTAVIPPKEKKPQATPPAPFQSPPTQRN  
 QRLKAANFKSEPRWDFEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFPLNLTFLDSRHF  
 NQSEWDRLEHFAPPFGFMELNYSLVQKVVTFRFPVPQQQLLASLPAGSLRCITCAVVGNGG  
 ILNNSHMQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFATAFSLTQSLILGNRGFKNVP  
 LGKDVRYLHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLHPDFL  
 RYMKNRFLRSKTLDGAAHWRIYRPTTGALLLTALQLCDQVSAYGFITEGHERFSDHYDTSW  
 KRLIFYINHDFKLEREVWKRLLHDEGIIRLYQRPGPGTAKAKN

**Cytoplasmic Domain:**

amino acids 1-10

**Type II Transmembrane Domain:**

amino acids 11-35

**Luminal catalytic Domain:**

amino acids 36-600

**Ribonucleotide Reductase small subunit Signature:**

amino acids 481-496

**N-glycosylation Sites:**

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

CGATGCGCGGACCCGGGCACCCCTCCTCCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCCG  
GAGCAGCGAGTGGAAATTGTTCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAAAACCT  
TACAGGCCCTCTTTATTTTAGTCAAAGTGCAGCAAACACTTCCATAGACTTTATCACAACA  
CCAGAGACTGCACCATTCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT  
GTCAGTCCAGTGTGATCGAGGATAAGTGAGCAGACCGGTACAGGAGCAGCACACCAGGAGCC  
ATGAGAAGTGCCTTGGAAACCAACAGGGGAAACAGAATATCTTTATACATATCCCTCATGG  
ACAAGAGATTTATTTTTCGACACAGACTCTTCCATAAGTCCTTTGAGTTTGTATGTTGTTG  
ACAGTTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTTATCTGTCACTTATTT

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**FIGURE 244**

MRGPGHPLLGLLLVLGFSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNT  
RDCTIPAYYKRCARLLTRLAVSPVCMDK

0990437.11501

**FIGURE 245**

GGGCTGGGCCCCGCCGACGTCCAGCTGGCCGGCTTGGTCTCGCGGTCCCTTCTCTGGGAGG  
CCCGACCCCGGCGCGGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCCGCGCCG  
CTCACCGCAATCGCTCTGTTGGTGTGGGGGCTCCCCCTGGTGTCTGGCCGGCGAGGACTGCCT  
GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTTCACCTTCT  
GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATACCGAGAGG  
CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT  
CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCTGTTGCTACCTGT  
ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTTGAAGGCCAGGAGATTCCAATGACAGGCATC  
CCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAGCTGGCCCTGCACCCCCACAGCC  
TGGCTTCATGTACCCACCTAGTGGTCTCTCCCAATATCCACTCTACCCAGCTGGGCCCC  
CAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC  
TGAGGAACCAGCCATGTCTCTGCTGCCCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT  
CCTGTACCTGCATCTGGTCTGGGGGTGGCAGGAGTCTCCAGCCACCAGGCCCCAGACCAA  
GCCAAGCCCTGGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGGAACAGGAGCTGAACTAGA  
ACTATGAGGGGTTGGGGGGAGGGCTTGAATTATGGGCTATTTTTACTGGGGCAAGGGAGG  
GAGATGACAGCCTGGGTACAGTGCCTGTTTTCAAATAGTCCCTCTGCTCCCAAGATCCCAG  
CCAGGAAGGCTGGGGCCCTACTGTTTGTCCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGT  
TCCGTCAGCAGCTGGCAGTAGCCCTCCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTG  
CTAGATTAAAGCTGTAAAGACAAA

000047.11001

**FIGURE 246**

MPPAGLRRRAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCCGTCYHRYC  
CRDLTLLITERQQKHCLA FSPKTIAGIASAVILFVAVVATTICCF LCSCCYLYRRRQQLQSP  
FEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYNPAAPPP  
YMPPQPSYPGA

**Transmembrane Domains:**

amino acids 10-28, 85-110

**N-glycosylation Site:**

amino acids 38-41

**N-myristoylation Sites:**

amino acids 5-10, 88-93

099043-1154  
10911-240660

**FIGURE 247**

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGGCGCAGGGTGAGGGCGGCCCCAGAA  
 CCCAGGTAGGTAGGCAAGAAAGATGGTGTCTGCCCCCAAAATGGTCCCTTGCACCACTG  
 TCATTTCTACTTTCTCACTTTGGCTCTCTTAAGTGTGTCACCTCCCTTCAATGTTGCAGAG  
 CACTGAAGCATCTCCAAACGCTAGTGATGGGACACCAATTTCTTGGAAATAAAAATGACACTTC  
 CTGAGTAGCTCATCCCAAGTCTATTATGATCTCTTGATCCATGCAAACTTACCACGCTGACC  
 TTCTGGGGAAACCCGAAAGTAGAAATACAGCCAGTCAGCCACAGCACCATCATCTCTGCA  
 TAGTCAACCACTGCAGATATCTAGGGCCACCTCAGGAAGGAGCTGGAGAGAGGCTATCGG  
 AAGAACCCTGCAGGTCTCTGGAACACCCCTCAGGAGCAAAATGCATGCTGGCTCCCGAG  
 CCCCTCTTGTGGGCTCCCGTACACAGTTGTCACTTCACTATGCTGGCAATCTTTCGGAGAC  
 TTTCCACGGATTTTACAAAAGCACCTACAGAACCAAGGAAGGGAACTGAGGATACATAGCAT  
 CAACACAATTTGAACCACTGCAGCTAGAATGGCTTTCCCTGCTTTGATGAACCTGCCTTC  
 AAAGCAAGTTTCTCAATCAAAATAGAAGAGAGCCAAAGGCACCTAGCCATCTCCAATATGCC  
 ATTGGTGAATCTGTGACTGTTGCTGAAGGACTCATAGAAGACCAATTTGATGTCACTGTGA  
 AGATGAGCACCCTATCTGGTGGCTTCATCATTTAGATTTTGAAGTCTGTGACGAAGATAACC  
 AAGAGTGGAGTCAAGGTTTCTGTTTATGCTGTGCCAGACAAGATAAATCAAGCAGATTATGC  
 ACTGGATGCTGGCGTGACTCTTCTAGAATTTTATGAGGATTATTTGACATACCGTATCCCC  
 TACCCAAACAAGATCTTGTGCTATTCCGCACTTTCAGTCTGGTGCTATGGAAAACTGGGGA  
 CTGACACATATAGAGATCTGCTCTGTTGTTTGAATGACAGAAAAGTCTTCTGCATCAAGTAA  
 GCTTGGCATCACATGACTGTGGCCCATGAACCTGGCCACCAAGTGGTTGGGAACTGGGTCA  
 CTATGGAATGGTGGAAATGATCTTTGGCTAAATGAAGGATTGGCCAAATTTATGGAGTTTGTG  
 TCTGTCAAGTGTGCCATCTGAACTGAAAGTTGGAGATTATTTCTTTGGCAATGTGTTTGA  
 CGCAATGGAGGTAGATGCTTTAAATTCCTCACACCTGTGTCTACACCTGTGGAAAACTCGTG  
 CTCAGATCCGGGAGATGTTTGGATGATGTTCTTATGATAAGGGAGCTGTATTTCTGAATATG  
 CTAAGGGAGTATCTTAGCGCTGACGCATTTAAAGTGGTATTGTACAGTATCTCCAGAAGCA  
 TAGCTATAAAAAATACAAAAACGAGGACCTGTGGGATAGTATGGCAAGTATTGCGCTACAG  
 ATGCTGTAAGAAGGATGGATGGCTTTTGTCTTAGAAGTCAACATTTCACTTCTCATCTCACAT  
 TGGCATCAGGAAGGGTGGATGTGAAAACCATGATGAACACTTGGACACTGCAGAGGGGTTT  
 TCCCTTAATACCATCACAGTGAGGGGGAGGAATGTACACATGAAGCAAGAGCACTACATGA  
 AGGGCTCTGAGCGCGCCCGGACACTGGGTACCTGTGGCATGTTCCATTGACATTTCACTCACC  
 AGCAATCCAACATGGTCCATCGATTTTGTCTAAAAACAAAAACAGATGTGCTCATCTCTCCC  
 AGAAGAGGTGGAATGGATCAAAATTTAATGTGGGCATGAATGGCTATTACATTTGTCATTACG  
 AGGATGATGGATGGGACTCTTTGACTGGCCTTTTAAAGGAACACACACAGCAGTCAGCAGT  
 AATGATCGGGCAAGTCTCAATTAACAATGCAATTTGAGCTCGTCAGCATTGGGAAGCTGTCCAT  
 TGAAGAAGCCTTGGATTTATCCCTGTACTTGAACATGAAACTGAAATATGCCCCGTGTTTTC  
 AAGGTTTGAATGAGCTGATTCCTATGTATAAGTTAATGGAGAAAAGAGATATGAATGAAGTG  
 GAACTCAATTTCAAGGCCTTCTCATCAGGCTGCTAAGGGACCTCATTTGATAAGCAGACATG  
 GACAGACGAGGGCTCAGTCTCAGAGCAAAATGCTCGGAGTGAACACTACTCTCTCGCTGTG  
 TGCACAACTATCAGCCGTGCGTACAGAGGGCAGAAGGCTATTTGCAAAAGTGGGAAGGAATCC  
 AATGGAAACTTTGAGCCTGCTGCTCGAGCTGACCTTGGCAGTGTGCTGTGGGGGCCAGAG  
 CACAGAGGCTGGGATTTTCTTATAGTAATATCAGTTTCTTTGTCCAGTACTGAGAAAA  
 GCCAAATTTGAATTTGCCCTCTGCAGAACCCAAAAATAGGAAAAAGCTTCAATGGCTACTAGAT  
 GAAAGCTTTAAGGGAGATAAAATAAAACTCAGGAGTTTCCACAAATCTTACACTATTGG  
 CAGGAACCCAGTAGGATAACCACTGGCCTGGCAATTTCTGAGGAAGAACTGGAAACAACTTG  
 TACAAAAGTTTGAAGTGTGGCTCATCTTCCATAGCCACATGGTAATGGGTACAACAAATCAA  
 TTCTCCACAAAGAACCGGCTTGAAGAGGTAAAAGGATTTCTCAGCTCTTTGAAAGAAAATGG  
 TTCTCAGCTCCGTTGTGCTCAACAGACAATTTGAAACCATTTGAAGAAAACATCCGTTGGATGG  
 ATAAGATTTTGAATAAATCAGAGTGTGGCTGCAAAAGTGAAGAGCTTGAACGTATCTGAAAAA  
 TTCTCCCTTCCCGGGTTTCTGTTATCTCTAATCACCACATTTTGTGAGTGTATTTTCAA  
 ACTAGAGATGGCTGTTTGGCTCCAACCTGGAGATCTTTTCCCTTCACTCATTTTTTGA  
 CTATCCCTGTGAAAGAATAAGCTGTAGTTTTCATGAATGGGCTTTTTCATGAATGGGCTA  
 TGCTACCATGTGTTTGTGTTTCTACACAGGTGTGGCCCTGCAACCTAAACCAAGTGTGGGT  
 TCCTTGCCACAGAAGAATAAAGTACCTTATTCTCTCAAAAAAATAAAAAAATAAAAAA

09990437.11501

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH  
YDLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPQLQVLE  
HPPQEQIALLAPEPLLVLPLPTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA  
ARMAFPFCFDEPAFKASFISIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVA  
FIISDFESVSKITKSGVKVSYVAVPDKINQADYALDAAVTLEFYEDYFISIPYLPKQDLAA  
IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHLELAHQWFGNLVTMEWWNDL  
WLNEGFAKFMFEFVSVSVTHPELKVGVGYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD  
DVSYDKGACITLNLMLREYLSADAFKSGIVQYLQKHSYKNTKNEIDLWDSMASICPTDGVKMGDG  
FCSRSQHSSSSSHWHQEGVDVKTMMTWTQLRGFPLITITVRGRNVHMKQEHYMKGSDGAPD  
TGYLWHVPLTFTITSKSNMVHRFLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL  
TGLLKGTHTAVSSNDRASLINNAFQLVSIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIP  
MYKLEMKRDMNEVETQFKAFLIRLLRDLIDKQWTDEGSVSEQMLRSLLELLACVHNYPQCV  
QRAEGYFRWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLSKYQFSLSTSEKSIQEFALC  
RTQNEKELQWLLDESFGDKIKTQEFFQILTLIGRNPVGYPLAWQFLRKNWNKLQVKFELGS  
SSIAHVMVGTTNQSTRFRLEEVKGFFSSLKENGSQLRCVQQTITETIENIGWMDKNFDKIR  
VWLOSEKLERM

amino acids 1-34

## amino acids 70-74, 154-158, 414-418, 760-764, 901-905

## amino acids 350-360



CAGGCCACAGACGGGTCTAGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCCA  
TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC  
GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTCCAGGA  
CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAAGCTTGGTGTCTCTCAAAGGCTGCACGG  
AGGCCAAGGACCAGGAGCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGAT  
TCCTACACCTTCGTGTGCGCGCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT  
TTGGGCCCCACAGCCCCCAGCAGACCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG  
AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCAAGGGGACCACACACTGTTATGAT  
GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC  
CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAGATTGGCCCGTGGTATGACTGAGA  
ACTGCAATAGAGAAAGATTTCTGACCTGTATCGGGGACACCATTATGACACACGGAAC  
TTGGTCTCAAGAACCCTATTGTTGGACACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT  
GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCTTGGTGGGGACAAAAG  
CTGTCAGCACTGTTGGGGCTCAAAAATCCAGAAGACCACCTCCACTCAGCCCCCTCTGGG  
GTGCTTGTGGCCTCCTATACCACCTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG  
CAGCGTTCGTCTGAACTCCCTCCCTCCTCAAGCTGCCCTGTCCAGGAGACCGGCACTGTC  
CTACCTGTGTGCAGCCCCCTTGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCAAG  
GGCGCCACTCATTTGTTATGATGGGTACATTATCTCTCAGGAGGTGGGCTGTCCACCAAAAT  
GAGCATTCAGGGCTGCGTGGGCCAACCTTCCAGCTTCTTGTGTAACACACCAGACAAATCG  
GGATCTTCTCTGCGCTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT  
GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG  
GTGGGGAGTGGTTTGCCCTTCTGCTACTCTATTACCCCCACGATCTTCCACCGCTGCTGA  
CCACCCCACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGACACCAGATCTTTTC  
CCATTCGTGCCATGAATCATCTTCCCAACACACCAATCATCTACTACCTAACAGCA  
ACACTGGGGAGAGCCTGGAGCATCCGGAATCTGCCATCTGGGAGAGGGGACGCTGGAGGATG  
CTGCATGTATCTGATAATACAGACCTGTCTCTTCA

MSAVLLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPQWTPKNTSCDSGLGCQDITLMLI  
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPLSLISYTFVCRQEDFCNNLVNSLPLWAPQP  
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTCHYDGLLRGGGIFSNLRVQGCMPPGCGN  
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSTNTEMCVEVGVCQETL  
LLIDVGLTSTLVGTGKGSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLNCSASSSVLLN  
SLPPQAAPVPGDRQCPTCVQPLGTCSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC  
VAQPSSFLLNHTRQIGIFSAREKRDVQPASQHEGGGAEGLESITWVGVLALAPALWGWVVC  
PSC

**FIGURE 251**

GCGACGGGCAGGACGCCCGTTTCGCCTAGCGCGTGCTCAGGAGTTGGTGTCCTGCCTGCGCT  
CAGG**ATG**AGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCACTGCTG  
CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCCTGCTCTGTGACATCCTCGTCCCTGG  
CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGACGGCCTGGAAGAGTCG  
GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTCGTCA  
GGAAAAATTGGTCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC  
TGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG  
AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCAATCAAGAATGCTGTCGCC  
GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA  
CGCCAGCTGTCCTGCCAGGGCGCGGGGGCACGCTGAGCATGCCAAGGACGAGGCTGCCA  
ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCCGTGCTTCATCGGCATCAAC  
GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCCATGCGGACCTTCAACAA  
GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGACTGCGTGGAGATGGTGGCCT  
CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG  
GAGAACATG**TGA**GCCTCAGGCTGGGGCTGCCATTGGGGGCCCCACATGTCCTTCAGGGTT  
GGCAGGACAGAGCCAGACCATGGTGCCAGCCAGGAGCTGTCCCTCTGTGAAGGTTGGAG  
GCTCACTGAGTAGAGGCTGTTGTCTAACTGAGAAAATGGCCTATGCTTAAGAGGAAAATG  
AAAGTGTTCTGGGTGCTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA  
ATGTCAATTATGTAATTATTACCCAGAATTGCTCTTCATAAAGCTTGTGCCTTTGTCCAAGC  
TATACAATAAAATCTTTAAGTAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAA

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**FIGURE 252**

MRGNLALVGVLISLAFLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGRVG  
PTGEKGDMDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLRKAIGE  
MDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMPKDEAAN  
GLMAAYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFNKWRSGEPNNAYDEEDCVEMVAS  
GGWNDVACHTTMYFMCEFDKENM

09900437.111501

**FIGURE 253**

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG  
 CACCAGTGTGTGAGGGGAGCAGGCAGCGTCTTAGCCAGTTCCTTGATCCTGCCAGACCACC  
 CAGCCCCCGGCACAGAGCTGCTCCACAGGCACC**ATG**AGGATCATGCTGCTATTACAGCCAT  
 CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG  
 TTCCTGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC  
 AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA  
 GGAATCAACATCTCCCAGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA  
 GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCCTCGGCC  
 CTTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC  
 TTTA**TAA**GACTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGT  
 ATCCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC  
 TTTCCCTGTCCCAATCCCAGGTGCGCAGCTCCTGTTACCTTTCTCTTCCCTGTTCTTGT  
 AACATCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCTGGTGTGGAACCTGCA  
 TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCTGTAGTGT  
 CCTACATTAAAAATATAATGTCTCTCTATTCTCAACAATAAAGGATTTTGCATATGAA  
 AA

0990437.11601

**FIGURE 254**

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK  
ALSQASTDPKESTSPEKRDHDDFFVGLMGKRSVQPEGKTGFFLPSVRVPRPLHPNQLGSTGK  
SSLGTTEEQRPL

**Important features:**

**Signal peptide:**

amino acids 1-18

**Tyrosine kinase phosphorylation site.**

amino acids 36-45

**N-myristoylation site.**

amino acids 33-39, 59-65

**Amidation site.**

amino acids 90-94

**Leucine zipper pattern.**

amino acids 43-65

**Tachykinin family signature.**

amino acids 86-92

109111 1240660

GGGGCTCTCCGGCTGCTCTCTATTAGACTGTCTGCTGCTGTGCCCGCTGTGCCCTGCTGTGCC  
CGCGCTGTGCGCGCTGCTACCGCGTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTG  
GAGCCCTGCGGAGAGCTCAAGCGCCCAGCTCTGCCCCAGGAGCCCAGGCTGCCCGTGTAGTC  
CCATAGTTGCTGCAAGGAGTGGAGCCATGAGCTGCGTCTCTGGTGGTGTATCCTCCCTTGGGGC  
TGCTGTTCTTGGTCTGCGGATCCCAAGGCTACCTCTGCCCCAACGTCACTCTCTTAGAGGAG  
CTGCTCAGCAAATACCAGCACAAAGAGTCTCACTCCCGGGTCCGAGAGCCATCCCCAGGGA  
GGACAAGGAGGAGATCTCTATGCTGCACAAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT  
CCAACATGAGGTACATGGTGAGCGCCGGCTCCGCGCCGAGAGGCTGGCACCGGGGGTGGGGC  
CTGGGCCACCAGCCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGCCTGTGATGG  
CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTTGTTGTTGTT  
TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAACTGCTATGCCCTG  
AAACCTTAGACTCCCGGGGTAAAGCATCCTGCTCAGCCTCCCAAGTAGCTGGAACCTACAG  
GCATGCACCATGGTGGCCAGCTAGATTATTTAAATTTTGTGGAGATGGGGTCTTGTCTACGT  
TGCCCAGGCTGGTCTTGAAGCTCTAGGCTCAAGCAATCTCTGCTCAGCCTCTCAAAGTG  
CTAGGATTATAGGACATGAGTCACCCCTGTCTGGCTCTGGCTCTGTTCTTAACATTCTGCCAAA  
ACAACACACGTGGGTTCCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACTCTTGGTAGC  
TCCACTGGGAACACAGCTCTCAGCCTTCCCACTGGAGGCAGAGTGGGGAGGGGCCAGGG  
CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCCTGACTTCTC  
CTTAGCCCGTGTGAGCCTCACTTTCCACTTGGAGAGTCTTCTCTCGCGTGGTGGCATGACT  
GTGAGATAAGTCGAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCAACCCCTAGG  
CTTTGCTAACCGGGAAAGAGGCTTAACGGTGACAGAAGACAGCCAAGGTCAACCCCTCCCGGT  
GATTGTGATGGGTGTTCCAGGTGTGTTTGGCGATGCTGCTACTTGACCCAAGCTCCAGTG  
TGAAACTTCTCTCTGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGTCTATCCGCT  
GTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTGAGTATGAATGGCTT  
TTTAAACAAACCCAGCTCCAGCCTGGGTAACTGTTAAAGCCCGCTCTACAAAAAATC  
CAAGTTAGCCGGGCGATGTGCTGCGACCTGTAGTCCCGCTGTCAGTGGGACTGAGGTGGAG  
GTGGAGTGGGGGGTGGGAGTCTGAGGAAGGAGGATCGTTGAGCCTGGGAAGTCGAGGCTGC  
AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCAAAA

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## **FIGURE 256**

MSCVLGGVIFLGLLFLVCGSQGYLLPNVTLLLELLSKYQHNEHSRVRRAIPREDKEEILML  
HNKLRGQVQPQASNMEYMVSAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGR  
GGSRLCSVLFVCFETGSHSATDAGVQWHNRHALKP

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **N-glycosylation site.**

amino acids 27-31, 41-45

#### **N-myristoylation site.**

amino acids 126-132, 140-146

#### **Amidation site.**

amino acids 85-89

0090437 11501



**FIGURE 257**

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**ATGGG**  
GTCTGGGCTGCCCTTGTCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGG  
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGC  
TTCTTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC  
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA**TGA**CAGCCATTGAAGCCTG  
TGTCTTCTTGGCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCTGTCTTT  
CAGCAGGCCCCCACCCTCCTGAGTGGCAATAAATAAAATTCGGTATGCTG

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**FIGURE 258**

MSGGLPLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSESSFLELLEKLCLLLHLPSTGTS  
VTLHHARSQHHVVCNT

09900437.11601

AATTGTATCTGTGTAATTGTTAAACAACAGAAATAAAATAGAAGGAAAACTTTCTGAGTTT  
CAAAAAACAACAGACTAGTACTCTAAAGAACTCTTTAAAACAATTAACTGTTAGGATTGCAGT  
**TATG**ATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTCTCTCCACTGTGTTCTGTGTGC  
TATTAATATTACCATTGCAGAAGCTTCATTAGTGTGAAATGAATGCTTAGTGGATCTG  
TGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTCCCCCTCC  
CTCGATTGTTCTAA**TAA**ATTGAAAGATGCTGCTGTGGAAAAGGCATGTATTTAAATCTG  
TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCCTTGAAAGCCAATGGAATACTTTTTTT  
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTGTTACGCTA  
GTAAATAGAAACCTGTGTTTATTCTCAGGTATTTAGAAACAACAGCCATCATTTTATTTT  
ATGTGTGTGTTCTTGGCTGTATTCTAAATTATATATTTGGGCTATCAAATATTACTTTCAT  
TCAATATAAATAACAATAGTAGAAGTTGTTACTTAGATATGCTTTCTAGTTGCATTTTCTC  
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGCTCTCTACTA  
TCTTCAGATTACTTGATTCAAATAACCAATTATGTTTGAATTTGATATTAATAAAACCAGA  
ATAAAAGTTCATATCTACCC

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**FIGURE 260**

MIGYYLILFLMWGSSTVFCVLLIFTTAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLP  
SDCSK

**Important features:**

**Signal peptide:**

amino acids 1-29

09990437.1.1601

GAGGATTTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACGGAGCCCTTGAGACATCCTT  
GAGAAAGGCCACAGCATAGAAGACATGCCCTGCTTGGAGTTTTTGACGAGATGTTGGCCCTT  
CGAGGAGCTTCTGCATCTGCTGTTCTGTTCTTGCAGCTTTTCTGCCCCGCCGAGCTGATC  
CCAGAGCCCGACATGTGTGATTCATTCATTCAGCCGCTTTCGAGTCTTGAGCAAGGGCTGG  
AAAAATGTACCCCAAGCAACGAGGCGATACATTCAGAAGTTCCAAAGGTTCTCAAAAATAATA  
TCTGTTCATGCTGGGAAGATGTGACACCTACACAAGTAGTACAAGAGTGAGTGGGTAACTT  
GGCATTGAGAGTTGAACGTGCCCAACGGGAGATGTGACTACATAACAATCACTTCAGAGGCTG  
ACAGGTGCATCGTATCAGAGGACAAGACATGGCAGAAATGTTGCTCCAAGAAGCTGAAGA  
GAGAAAAGATCGCGACTCTGCTGAATCGAAGCTGTGACAACTGCTGATGGGCAATAAAGT  
TTTGAAATAGTGAAGAAGATGATGACACACATGGCTCTTGAGTAGAAGATGCTGCTTATA  
ACTCTCCAAGGTTGATCTTATTAATTTGGATCCGAAACAACACTGTTTGGGAATTTGCAAC  
ATACGGGCACTTCATGAGGATAAACCAAGCAGCTCCCGGAAGCAAACTCTAACACTTTC  
CTGGCAGGGGAACAGGCCAAGTGATCTCAAAAGTTTTCATTTTTCAATAACCAAGCAACT  
CTAATGAGATAATCAAAATAAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGTCCCA  
GGAGGCTAGGCCGAGCATTTGTTTACCAGCACTCCCCTCAACTTACATTGACCTGGCTGT  
GGATGAGCATGGGCTCTGGGCCATCACTCTGGGCCAGGCCACCATAGCCATTTGGTTCCTCA  
CAAGATTTAGCGCGGCCACACTGGGAGTGAGCAATTCTGGGATACCCATTGCAAGAAGCCAG  
GATGCTGAAGCCCTCATTTCTCTTGTGTGGGTTCTCTATGTGTCTACAGTATGGGGGCCA  
GGGCCCTCATGCGATCACTGCATCTATGATTCACCTGGGCATATCAGTGAGGAGGAATTCG  
CCAACCTGTTCTTCCCAAGAGCAAGGAAGTCACTCATGATTCATTACACCCCAAGAGAA  
AAGCAGCTCTATGCTCGAATGAAGGAACACAGATCACTTTTCAAACTCCAGACAAGAGAAA  
GCTGCTCTGAACTTAAGTCATTACAGCTGTGAGAAAGAGCACTGTGGCTTTTGGCAGCTGTT  
TACAGGACAGCTGAGGCTATAGCCCCCTCAAAATATGATATCCCTCTAATCACACAGGAAG  
AGTGTGTAGAAGTGGAAATACGTATGCTCTTTTCCAAAGTGTCACTGCCTTAGTATCTTC  
CAAGAGCTTAGATGAGGACATATCATCAGGAAGTTTCAAAATGTCCATTACTCCCCAAA  
CTCTCTGGCTCTCAAGGATGACCACATTCTGATACGCCATCTTCAAGCCTTTTGGTTTAACT  
GCTCCCCAGCTATTACTGTAACTTGCCATCTCCCTCCCAACTATGAGTTGTATGCGCAGC  
CCATTAATTCACCACCTGGCTTTTCTCTCCCTGGCCTTTGCTGAAGCTTCTCCCTCTTTT  
CAAAATGCTATTTGATATTCTCCATTTTCACTGCCCACTAAATACTATTAAATATTTCTTT  
CTTTTCTTTCTTTTTTTGGAGACAAGGCTCACTATGTTGGCCAGGCTGGTCTCAAACCTC  
AGAGCTCAAGAGATCTCTCGCTCGCCAGGCTCCTAAGTACTGGGATACAGGCATGTGCCAC  
CACACTGGCTTAAATACTATTCTTTATGAGGTTTAACTCTATTTCCTACGCTGCCCTGTC  
TCTTCACTAAGCTTGGTAGATGTAATAAAGAGTGAATAATTAACATTTGAATATGCTGTT  
CCAGGTTGTGAGTGTTCATGACATTTAAATCTCGTTTCACTTTGTGTAACATGCACAG  
TCTTTACAGCTGTCACTCTAGAGTTTAGGTGAGTACACAATTAACAAGTGAAGATACAGC  
TAGAAAACTACAAATCCCATAGATTTTTCATTGCCCAAGGAAGCATCAAAATCGATATGTT  
TGTTCACTCACTCTCTATAGTCAATGCTGTTCTATGCTTCAAGCTTAAATATGATGCTGCTC  
TTTAGCAGCTTTTATGCTGTCACAAGACCTTTCAATAGGCTTTCAATGATAAATTTCTCC  
AGAAAACCAAGTCTAAGGTTGAGGACCCCACTTACGCTCTCTTGTCTGCTGCTCTGCTGT  
TCTCTCTTCTGCTTTAAATTCATAAAGTGACACTGAGCAAAAAA

**FIGURE 262**

MMVALRGASALLVLFLLAAFLPPPQCTQDPAMVHYIYQRFRVLEQGLEKCTQATRAYERFQE  
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQRIDYIQYLREADECIVSEDKTLAEMLL  
QEAEKEKKIRTLNASCNMLMGIKSLKIVKKMMDTHGSWMKDAVYNSPKVYLLIGSRNNTV  
WEFANIRAFMEDNTKPAPRKQILTLWQGTGQVIYKGFLLFFHNQATSNEIIKYNLQKRTVED  
RMLLPGGVGRALVYQHPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEIPGTLGVEHSWDT  
PCRSQDAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLEFFPKRPRSHSMIH  
YNPRDKQLYAWNEGNQIIYKLQTKRKLPLK

0000437 115611



MELSQMSELMGLSVLLGLLAMATAAVARGWLRAGEERSGRPACQKANGFPDPKSSGSKKQK  
QYQRIKKEKPPQHNHFRLLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ  
REHRSMRANVELDHATLVRFPDCRAFIWVLANGDTLRVFKMTKREDDGGYFTATPEDFEKK  
HKAPVIDIGIANTGKFIMTASSDTTVLIWSLKGQVLSTINTNQMNNTHAAVSPCGRFVASCG  
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV  
EYKKKQDPYLLKTRFEEAAGAAPCRLALSPNAQVLALASGSSIHLNTRRGEKEECFERVH  
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHKLKASNESTRQRLQQQLTQ  
AOETLKSGLAKK

Signal peptide:

amino acids 1-25

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308



TGGCTCTCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG  
CAGTGTTTTGCCTTCACCCCAAGTGACCATGAGAGGTTGCCACGCGAGTCTCAATCATGCTCC  
TCCTAGTAACCTGTGCTGACTGTGCTGTGATCACAGGGGCCCTGTGAGCGGGATGTCCAGTGT  
GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCT  
GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCTTCTTCAGGAAACGCA  
AGCACACACCTGTCTTGTCTTGCCAACCTGCTGTGCTCCAGGTTCCCGGACGCGAGGTAC  
CGCTGCTCCATGGACTTGAAGAACATCAATTTTTAGCGCCTTGCCTGGTCTCAGGATACCCA  
CCATCCTTTTCTGAGCACAGCCTGGATTTTTATTCTGCCATGAAACCCAGCTCCCATGAC  
TCTCCAGTCCCTACACTGACTACCTGATCTCTCTTGCTAGTACGCACATATGCACACAG  
GCAGACATACCTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTACAGCTTGAGG  
CTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTTGTA  
AATGGCAGAAAGGACATTTCCCCCTCCCTCCCCAGGTGACCTGCTCTCTTCCCTGGGCCCTG  
CCCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTTGGGT  
GCATTGCTCAGAGTCCCAGGTCTTGCCCTGACCTCAGGCCCTTCACGTGAGGTCTGTGAG  
ACCAATTTGTGGGTAGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC  
TCAAGATTGGCTCTTCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA  
GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCAGTCAGCCTGTGGCTTGTGGCCTGTGA  
CCTGTGACCTTCTGCCAGAATTGTGATGCCTCTGAGGCCCTCTTACCACACTTTACCACT  
TAACCACTGAAGCCCCCAATTCCACAGCTTTTCCATTAAAAATGCAAAATGGTGGTGGTTCAA  
AGGATCAGCCCTGAGAGCAGGTGTGGTGACTTTGAGGGAGGCAGTCTCTGTGCCAGATTGGGG  
TGGGAGCAGGGGACAGGAGCAGGGCAGGGGCTGAAAGGGGCACTGATTAGACCAGGGAGG  
CAACTACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAAA

**FIGURE 266**

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAI SLWLRGLRMCTPLGREGEECHP  
GSHKVPFFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

**FIGURE 267**

AGCGCCCGGGCGTCTGGGGCGGTAAGGCCGGCAGAAAGGAGGCACCTTGAGAAATGCTCTTTCTCCAGGACCCAAAGTTTCTTACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGCTGCTGCCTTGGCATTGCTGCTTGCCAAACACAGACGTGTTCTGTGTCCAAGCCCCAGAAAGCGGCCCTGGAGTACCTGGAGGATATAGACCTGAAAAACACTGGAGAAGGAACCAAGGACTTTTCAAGCAAAGGAGCTATGGGAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTTCTCTGTGAGAGGAAGCTGCGGATCTGTCTCCCTGAAAAGCATGTTGGACCAGCTGGGCGTCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTATTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCGGAAGATGATGTTTATGGGATTTATCCGTCTGGGAGTGTGGTACAACCTTCTCCGAGCCTGGAACGGAGGCTTCTCTGGAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCGTGGTGGGATCAGGAAGCAGGGCATTCTTCTTGAGCACCGAGAAAAAGAATTGGAGACAAAGTAAACCTACTTCTGTCTGGAAGCTGCTAAGATGATCAAAACCACAGACTTTGGCCTCAGAGAAAAATGATGTGTGAAACTGCCAGCTCAGGGATAACAGGGACATTCACCTGTGTTTCATGGGATGTATTGTTTCCACTCGTGTCCCTAAGGAGTGAGAAACCATTTATACTCTACTCTCAGTATGGATTAATAATGTATTTAATATTCTGTTTAGGCCCACTAAGGCAAAAATAGCCCCAAAAACAAGACTGACAAAAATCTGAAAACTAATGAGGATTATTAAGCTAAACCTGGGAAATAGGAGGCTTAAATTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCCAAGGTGAGCAAGTCACTTGAGGTCGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTCTCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGTACCCGGGAGGCTGAGGCAGGAGAATCACTTGAACTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCAACCACTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

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**FIGURE 268**

MSFLQDPSFFTGMWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTLEKEPR  
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKMLDQLGVPLYAVVKEHIRTEVKDF  
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEFILGGVFV  
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

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**FIGURE 269**

ACCGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCG  
GGCCAGGTGCCCCGTCGAGGTGCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA  
AGCCCCCTTCTCGGCGTGCCAAACCGGCCACCCAGCCATGCGGAACCCGGGCTGGGGCTG  
CTTCTGGCGCTGGGCTGCCGTTCTGCTGGCCGCTGGGGCCGAGCCTGGGGGCAAATACA  
GACCACTTCTGCAATAGAAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG  
GCAACCTCGGTCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCGCTTG  
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG  
CACCTACCGGCCAGTAGCGAGGAGCAGTTCTCCCATGACGCCGAGGCCCGGGCCCTCAGG  
ACTCCAAGGAGACGGTGACGGCTGCCCTGCCCATTAGCTCCCTCTCTGTCATCTGTCTTC  
CTTCATTGCTGTGTGACCTTGGGAAAGGACATGCCCTCTCTGGGACGTCAGATCCACCCAG  
TGCTTAAATAGCAGGAAGGACTACTTCAAAGACTTGCCCTGAGGTCAAGAGAGGATGGG  
GCTATTACGCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAA

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**FIGURE 270**

MANPGLGLLLALGLPFLLARWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIV  
VFSLAALLLAVGLALLVRKLRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

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**FIGURE 271**

AATATATCATCTATTTATCATTAATCAATAATGTATTCCTTTATTCGAATAACATTTGGGT  
TTGGGATTTTAATTTTCAAACACAGCAGAATGACATTTTTCTGTCACTATTATTATTGTTG  
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT  
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC  
CTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA  
GGGTTAATTCTTGGTGTCTGAAGCCTGGGGCAGGGGTGTAAGAAAAACACTTAGATTCAATG  
ATTGTAAATTTAAGGCAATACACATATTAGTATTACCTTAGTGAATGTATCCCTGTCATA  
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT  
TTATTAATTTTAAATCAGTAACTGATTATCACTGGCTATGTGCTTAGATCTACAGGAGA  
TCATATAATTTGATACAAATAAAAGAAAAGTGTCTCTCCCTTACAGAATTGACATTTTAA  
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA  
AGAAGGGAAAATGTTGCCAAGGAAAAAAA

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**FIGURE 272**

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK  
GIVKGRNLDSRGLILGAEAWGRGVKKNT

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**FIGURE 273**

GCCAGGAATAACTAGAGAGGAACA**ATG**GGGTATTTCAGAGGTTTGTTCCTCTTAGTTCT  
 GTGCCGTGCTGCACAGTCAAATATCTCCTTCATTAAAGCTGAATAATAATGGCTTTGAAGATA  
 TTGTCATTGTTATAGATCTCTAGTGTGCCAGAAGATGAAAAATAATTGAACAAATAGAGAT  
 ATGGTCACTACAGCTTCTTACGTACCTGTTTGAAGCCACAGAAAAAGATTTTTTTTCAAAAA  
 TGTATCTATTAATTCTCTGAGAATTGGAAGGAAAAATCCTCAGTACAAAAGGCCAAACATG  
 AAAACCATAAACATGCTGATGTTATAGTTGCACCACTACACTCCAGGTAGAGATGAACCA  
 TACACCAAGCAGTTACAGAATGTGGAGAGAAAGCGAATACATTCACTTCAACCCTGACCT  
 TCTACTTGGAAAAAAACAAAATGAATATGGACCACAGGCAAACTGTTTGTCCATGAGTGGG  
 CTCACCTCCGGTGGGGAGTGTGTTGATGAGTACAATGAAGATCAGCCTTTCTACCGTCTAAG  
 TCAAAAAAATCGAAGCAACAGGTGTTCCCGCAGGTATCTCTGGTAGAAATAGAGTTTATAA  
 GTGTCAGGAGGCCAGCTCTCTTAGTAGACATGCAGAATTGATTTCAACAAAAAACTGATG  
 GAAAAGATTGTAATTCTTCTCTGATAAAGTACAAACAGAAAAAGCATCCATAATGTTTATG  
 CAAAGATTGATCTGTTGTTGAATTTTGTAAACGAAAAACCCATAATCAAGAAGCTCCAAG  
 CTAACAAAAACATAAAGTGAATTTTGAAGTACATGGGAGGTGATAGCAATTTCTGAGGATT  
 TTAACAAACCATACCTGTTGACACCACCTCTCCACCTGTCTTCTCATTTGCTGAAGATC  
 AGTCARAAAGATTGTGCTTAGTTCTTGATAAGTCTGGAAGCATGGGGGGTAAAGACCGCT  
 AAATCGAATGAATCAAGCAGCAAAAACATTTCTGCTGCAGACTGTTGAAATGGATCTCTGGG  
 TGGGGATGGTTCACTTTGATAGTACTGCCACTATTGTAATAAGAGCTAATCCAAATAAAAAAGC  
 AGTGATGAAGAAGAACACACTCATGGCAGGATTACCTACATATCTCTGGGAGGAATCTCCAT  
 CTGCTCTGGAATTAATAATGCTATTCAGGTGATTGGAGAGCTACATCCCAACTCTGATGGAT  
 CCGAAGTACTGCTGCTGCTGATGGGGAGGATAACACTGCAAGTCTTGTATTGATGATGAAGT  
 AAACAAGTCTGGGCCATTCTCATTATTTATGCTTTGGGAAGAGCTGCTGATGAAGCAGTAAT  
 AGAGATGAGCAGAGATAACAGGAGGAAGTCAATTTATGTTTCAGATGAAGCTCAGAACAATG  
 GCCTCATTTGATGCTTTTGGGGCTCTTACATCAGGAAATACATGATCTCTCCAGAAAGTCCCTT  
 CAGCTCGAAAGTAAAGGATTAACTGAATAGTAACTGCTGGATGAACGACACTGTGTAAT  
 TGTATGATCAGTGGGAAAGGACAGCTTCTTCTCATCACATGGAACAGTCTGCTCTCCAGTA  
 TTTCTCTCTGGGATCCCATGGAAACATAATGGAATAATTCACAGTGGATGCAAGTTCCAAA  
 ATGGCCTATCTCAGTATTCCAGGAATGCAAGGTGGGCACCTTGGGCATACAATCTTCAAGC  
 CAAAGCAACCCAGGAACATTAACATTTACAGTAACTTCTCGAGCGCAAAATTTCTCTGTG  
 CTCCAATCACAGTGAATGCTAAATGAATAAGGACGTAACAGTTTCCCAGGCCAATGATT  
 GTTTACGCAGAAATTTCTACAAGGATATGTACCTGTTCTTGGAGCCAATGTGACTGCTTTTAT  
 TGAATCACAGAAATGGACATACAGAAGTTTGGAACTTTTGGATAATGGTGCAGGCGCTGATT  
 CTTTCAAGAAATGATGGAGTCTACTCCAGGTATTTACAGCATATACAGAAAAATGGCAGATAT  
 AGCTTAAAGTTTCGGGCTCATGGAGGAGCAACACTGCCAGGCTAAAAATACGGCCTCCACT  
 GAATAGAGCCGCGTACATACCAGGCTGGGTAGTGAACGGGGAAATTTGAAGCAACCCGCCAA  
 GACCTGAAATTTGATGAGGATACTCAGACACCTTGTGGAGATTTCAGCCGAACAGCATCTCCGA  
 GGTGCATTTTGGGTATCACAAGTCCCAAGCTTCCCTTGCTGACCAATACCCACCAAGTCA  
 AATCACAGACCTTGATGCCACAGTTTATGAGGATAAGATTATTTCTTACATGGACAGCAGCAG  
 GAGATAATTTTGTGTTGGAAAGTTCAACGTTATATCATAGAATAAGTGCAGATTTCTT  
 GATCTAAGAGACAGTTTGTGATGCTCTTCAAGTAAATACATCTGATCTGTCAACCAAGGA  
 GGCCAACTCCAAGGAAGCTTTGCATTAAACAGAAAAATCTCAGAGAAAGATGCAACCC  
 ACATATTTATTTGCCATTAAGTATAGATAAAAGCAATTTGACATCAAAAGTATTTCCAACTT  
 GCACAAGTAACTTTGTTTATCCCTCAAGCAATCTGATGACATGATCTACCTACCTCTCC  
 TACTCTTACTCTACTCTCTGATAAAAGTCAATTTCTGGAGTTAATTTTCTACGCTGGTAT  
 TGTCTGTGATGGGCTGTTGTAAATGTTAACTTTATTTAAGTACCCACTTT**TC**AACCTTA  
 ACCAAGAAAAAATCTTCAAGTAGACCTAGAAGAGAGTTTAAAAAACAACCAATGTAAAT  
 AAAGGATATTTCTGAATCTTAAATTCATCCCATGTGTGATCATAACTCAAAAAATAAT  
 TTAAGATGTCGGAAGGATACTTTGTATTAATAAAACACTCATGGATATGTAAGAACTGT  
 CAAGATTAAATTTAATAGTTTCATTATTTTATTTGTAAGAAATAGTGAATGAC  
 AAAGATCCCTTTTCTACTGATACCTGTTTGTATATTTTGAATGACAGTGTCTGTAAT  
 GATATTTCAATTTGATCAAGAAATTAATATCATCTAGTGTGATGATCAAAATACAGTAAA  
 GGAGAGCAAAATAACAACATTTGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAA  
 AA

**FIGURE 274**

MGLFRGFVFLVLLCLLHQNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIEQIEDMVTASTY  
 LFEATEKRFFFKNVSLIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTEC  
 GEKGEYIHFTPDLLLGGKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR  
 CSAGISGRNRVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDQVQTEKASIMFMQSIDSVVE  
 FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPPVFSLKISQRIVCLV  
 LDKSGSMGGKDRNLNRMNQAAKHFLQTVENGSSWVGMVHFDSTATIVNKLIIQIKSSDERNTLM  
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLLTDGEDNTASSCIDEVKQSGAIVH  
 FIALGRAADEAVIEMSKITGGSHFYVSDEAQNGLIDAFGALTSGNTDLSQKSLQLESKGLT  
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSTIMENFTVDATSKMAYLSIPG  
 TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKMKNKDVNSFPSPMIVYAEILQG  
 YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNKDVYSRYFTAYTENGYSLSKVRAGH  
 GANTARLKLRPPLNRAAYIPGWVVNGEIEANPPRPEIDEDTQTTLLEDFSRASGGAFFVVSQV  
 PSLPLPDQYPPSQITDLDTVHEDKIIILTWTAPGDNFVGVQRYIIRISASILDLRDSFDD  
 ALQVNTDLSPEKANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNNIAQVTLFIP  
 QANPDDIDPTPTPTPTPKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

**Signal peptide:**

amino acids 1-21

**Putative transmembrane domains:**

amino acids 284-300, 617-633

**Leucine zipper pattern.**

amino acids 469-491, 476-498

**N-glycosylation site.**
 amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,  
 628-632, 811-815, 832-836, 837-841, 852-856, 896-900

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**FIGURE 275**

CTCCTTAGGTGGAACCTGGGAGTAGAGTACTGACAGCAAAAGACCGGGAAAGACCATACGTCCTCCG  
 GGCAGGCTGTACCAACAGGTGTCACTTTTGTGATCTCGTGTGTGGCTGCCTTCTCATTTTCAAGSAAAG  
 AGCCCAAGGTAAATTTTGACCAGAGGAGCAATGATAGCCACCTCTTAACCTTCCCTTTCTGAAACC  
 CCCAGTTATGCCAGGATTTACTAGAGAGTGTCAACTCAACCAGCAAGCGGCTCCTTCGGCTTAACCT  
 TGTGGTTGGAGGAGAGAACCTTTTGTGGGGCTGCGTTCTCTTAGCAGTCTCAGAAGTGTCTGCTGTA  
 GGGTGGACGAGAGAAAGGAAGGATCCCCCTTGTGCTTGGCTGCACATCGCAAGGAGCTGTGATGGG  
 AATGAGAGTGAACACTTTGGAGATTTCACTTCAGTCAATTCGCTTCGCTCGACATGACCTTTTAAAA  
 GTAGAGAAGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGAGCAGACTCGTCTAGAGAGGAATGCAT  
 CAAGCAGCTCCGGGGGCCCAAAACGCATGCTTCTGTGGTCTAGCCCCAGGAGCCTTCCGTGGG  
 GCCCCGGCTTTGAGGGATGCCACCGGTTCTGGAGCGATGGCTGATTTCTGATGATGTTTGGC  
 GGGGGCTGCTTTCGTGGATTTCCGGGTGGTAAATTTTGTCTGGTCTCTTCTGCTGGCTATCTCTGT  
 CCGTGTACATGTTGGGCTGCACCCCAAGGTGACGAGGACACTGGCCTCTGCTGGCTATCTCTGT  
 CCTCAGGGGAAGGAGGGTACCCCAAGGTGACGAGGACACTGGCCTCTGCGGAGGCCAACAGC  
 GAGCGCTGAAGCGGAGATGCGACAGCTCAAGGAGGAGCTGCAGGAGGAGGTGAGCAGCTCAGGAA  
 TGCGCAGTAGCAACGAGCCGATGCTGCTGGCCTGGGCTGCGAGGAGGCCCCCCAGGAGAAACCCAG  
 GCCAGCTTCTTGGCTTCTGCTCACTCGCAGGTGGACAAGGCAGAGTGAATGCTGGCGTCAAGCTG  
 CCACAGAGTATGACGAGCTGCTTTCGATAGCTTTACTCTACAGAGAGGTGTACCAGCTGGAGACTGG  
 CCTTACCCGACACCCGAGGAGAGCGCTGTGAGGAAGGACAAGCGGATGAGTTGGTGGAGGCCAT  
 GAATCAGCTTGGAGACCTTGAACAATCCTGCAGAGAACAGGCCAATCAGCGTCTTACACGGCTCT  
 CTGATTTTCATAGAAGGATCTACCGAAGCAGAAAGGGACAAAGGGACATTTGATGAGCTCACTTCAA  
 AGGGGACCAACCAACGAAATTCACACGGCTCATCTTATTTCCGACCATTCAGCCCCATCTGAAGT  
 AAAAAATGAAAGCTCAACATGGCCACAGCTTATCAATGTTATTCGCTCTGAGCAGTGTGAGTGGG  
 ACAAGTTCGGGAGCTTATGACAGAAATTCAGGGAGATGTGCTGATGAGCAGGATGAGGAGTGGG  
 CACTGTTGTTTACTTTTGGAGAGGATTTCTCATCAGCTGAATGGAGAAATTTCTCGGGGAGAGGACTG  
 GCTGCGCACTTCAGGAATCTTACCTTATCCAGGAGGAAGCAAGCTCCTTCTCTTTTCTGTGATGTGACATCTTACTT  
 ATGTTGGAGCCCGCTTCTGGAAGGGAAGCAAGCTCCTTCTCTTTTCTGTGATGTGACATCTTACTT  
 CACATCTGAATTTCTCAATACGTGTAGGCTGAATACACAGCAGGGAAGAGGATTTTATTTACGAT  
 CTTTTCAGTCACTAAATCCTGGCATAATATACGGCCACCATGATGAGTCCCTCCTTGGAGACAG  
 AGCTTGGTCATAAGAGAGAAAGCTGGATTTGGAGAGACTTTGGATTTGGGATGACGTTGCAATG  
 GTCAGACTTTCATCAATATAGTGGGTTTGTCTGAGACATCAAGGCTGGGGCGGAGAGGATGTGCAC  
 CTTTATTCGCAAGTATCTCCACAGCAACCTCATAGTGGTACGGAGCGCTGTGCGAGGACTCTTCCAC  
 TCTGGCATGAGAGGCGCTGCATGGACGAGCTGACCCCGAGCAGTACAAGATGTGATGAGTCCAA  
 GGCCATGAACAGGCGATCCACCGCCAGCTGGGATGCTGGTGTTCAGGACAGAGATGTGSGAGA  
 CACTTTTCTTCTTCTTTTGCATTTCTGAAATCTGAAAGTGGCTGCACAGAGAAAGACTTCCATGAAGGAGC  
 ACAAAAGAAATGGAGCTGATGGGTGAGAGTGGCTGCACAGAGAAAGACTTCCATGAAGGAGC  
 AACAGAAATCAAAATCCCGCTTTGCTGCAAAAGTAAACAGTGTGACGTTTGCATGTGGAAGTGTCTGACA  
 TAGGCAGATGCTGTGAGATTTAAGCCTAATGGTGTGGAGTTTTCATGGTGTTTACATACACT  
 GAGCCTGTGTTTGTGTGCTCATTGAAATATTCATGATTTAAGAGCAGTTTGTGTAATAAATTCAT  
 ATGACTGAAGGCAAGCATTTTCTCCTCATATGAATGAGCTATCAGGAGGCTGATTTCTCTTAGG  
 AATGCTAAATATTCAGAAGGCGAGGAGAGATAGGCTTATATGATAGTACTAGTGAATATTAAGTA  
 AAATAAAATGAGGACCAAGAAAGAAAGCAACATAAATATCGTGTATATTTTCCCAAGATTAAACA  
 AAAATAATCTGCTATCTTTTGGTGTCTTTTAACTGTCTCGGTTTTTCTTTTATTTAAATAAT  
 GCACTTTTTTCCCTTTGTGAGTTATAGTCTGCTTATTTAATACCACCTTGCAGGCTTACAAGAGA  
 GCACAAGTTGGCTCAATTTTATATTTTTTAAGAAGATCACTTTGAGATGCATTTAGACACTTCA  
 GTTCAAAGCATACAAATTTGATGCCATATCCAAGGACATGCCAAATCTGCTCTCAGGACCAAT  
 GTCCAGGACTGAGACATAGGGAAGGAATGGTTTGTACTAATACAGACTGACACTTCTGCTTTCTGAA  
 GAGTATTTTCGAGAGGAGGCACTGACACTGGAGCAAGAAATGAGACTGACACTTCTGCTTTCTGAA  
 AAGGAACCTTTACAGCTGTGATATCTGATGTAACCTAAGTACCTGATTTCTCTCAGGACCAAT  
 GAAGTAGGAGCCGCTTCTTACTCTTTAAATAAACCAGATATACCGTGTGAGACCAACCAATCTCT  
 TTTCAAAACAGGCTGCTCTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT  
 ATATATATATATGTCGAAGAGTCAATCCATCTGCGAGAACTAGTGGGATGGAAGTTTGTGCTACAT  
 GTTATCCACCCCAAGGAGGAGTAAGTAACTGAATTTATTTTAAATTAAGCACTTCTACTCAATCA  
 CCAAGATGCTTCTGAAATTTGATTTTATTTACCTTTTCAAACTATTTTAAATAAATACAGTTA  
 ACATAGAGTGGTTTCTTCACTATGTAATTTATGAGGACCAAGTACAGTACGATGCTAATTTCT  
 CTTTGTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT  
 TGTGCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT  
 AGGCCATGAATGGAAGTGGTATTCGACAGCTAATAAATATGATTTGTGGATATGAA

**FIGURE 276**

MMVVRGLLAWISRVVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQ  
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL  
HSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVRKDKRDELVEAIES  
ALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTYELTFKGDHKHEFKRLILFRPFSP  
MKVKNEKLNMANLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK  
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR  
LNTQPGKKVFYPVLFQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI  
NIGGFDLDIKGWGGEDVHLYRKYLHSNLIVVRTPVRLFLHLWHEKRCMDELTPSEQYKCMQ  
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

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GGAAGAATGTTGTGGCTGCTCTTTTTCTGGTGACTGCCATTATGCTGAACCTGTCAACAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTCTCCATGAGAAAAATTCCCAACAGAGAAGCAACAGAAAATTTCCCATGTCTACTTTGCAATGTAACCCAGAGGGTATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCTGCTGTTGAGGTGC AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACCTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACACTACTGATTTTAT CAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT AAGTGTGAAAACATGATCACAAATGAAAAATGGCATCCCCCTCTGATCCCCCTGGACATGAAGGG GGGCATATTAATGATGCCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT TGTTCCTGCTTCTCAAGAAATTAACATTGTTTCTGTGTGACTGCTGAGCATCTGAAATA CCAAGAGCAGATCATATATTTTGTTCACCAATCTTCTTTTGAATAAAATTTGAATGTGCT TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGAC TCAAAATATPCTAAAATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG TAGTTATTGATTTAAGCATTTTTAGAAAATAAGATCAGGCATATGTATATATTTTCACACTTCAAAGACCTAAGGAAAAATAAAATTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT TGAAAATGGATCCTTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAACAAAAG TGAGAAGTAATTATTGTAATGGATGGATAAAATGGAATTACTATACAGGGTGGAAATT TATCTCTGTTATCACACCAACAGTTGATTATATATTTCTGAAATATCAGCCCTAATAGGAC AATTCATATTTGTGACCAATTTTACAATTTGTAAAGATCCAATCTGTGCTAACTTAATAAAG TAATAATCATCTCTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 278**

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP  
NREATEISHVLLCNVTQRVSFVVDPSKNHTLPAVEVQSAIRMKNRINNAFFLNDQTL  
FLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLLSGIWQRRRKNKEPSEVDDAEDKC  
ENMITIENGIPSDPLDMKGGILMMP

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**FIGURE 279**

AACTCAAACCTCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGAGTGCCCTTGGCAGG  
 GTGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTC**ATGT**  
 ATGGCAAGAGCTCTACTCGTGGGTGCTTCTTCTCCTTGGCATACAGCTCACAGCTCTTTGG  
 CCTATAGCAGCTGTGGAAATTTATACCTCCCGGTGCTGGAGGCTGTTAATGGGACAGATGC  
 TCGGTTAAAATGCACCTTTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACCTGGA  
 ATTTTCGTCTCTAGACGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC  
 CAACCCATGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGA  
 TGCCTCCATCCTTCTCTGGAAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA  
 AGAACCACCTGATGTTGATGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA  
 CGCTTCTCTGAGATCCACTTCTTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT  
 AATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC  
 ATAAAGTGGTGGAGATAAAATCAAAAGAAGAGGAAAGGCTCAACCAGAGAAAAAGGTCTCT  
 GTTTATTTAGAAACACAGACT**TAA**CAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACAA  
 GAACCCTAGTATTTCTTGAAGTTAATGGAACCTTTTCTTTGGCTTTTCCAGTTGTGACCCGT  
 TTTCCAACCAAGTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC  
 AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTTAAGGTCTTATTTAATTTTCA  
 GTGTAATTTTTTCAAGTGCTCATTAGGTTTTATAACAAGAAGCTACATTTTTGCCCTTAA  
 GACACTACTTACAGTGTTATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCC  
 AATTTGTCTGTATACATTTCCCTTTCACGTATTCTTTTAGCAGCACTTCTGCTACTAAAGTTA  
 ATGTGTTTACTCTCTTCCCTCCACATTCTCAATTAAGGTGAGCTAAGCCTCCTCGGTG  
 TTTCTGATTTAACAGTAAATCCTAAATTCAACTGTTAAATGACATTTTTATTTTATGTCTC  
 TCCTTAACATATGAGACACATCTGTTTTACTGAATTTCTTTCAATATTCCAGGTGATAGATT  
 TTTGTGC

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**FIGURE 280**

MYGKSSTRAVLLLLGIQLTALWPIAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDAITVT  
WNFRPLDGGPEQFVFYYHIDPFQPMSEGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ  
VKNPPDVGVIIEIRLSVVHTVRFSEIHFLALAIQSACALMIIIVVVVLFQHYRKKRWAER  
AHKVVEIKSKEERLNQEKVSVYLEDTD

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**FIGURE 281**

GCATTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGT  
ACTCTTGGGAGTTTCCATCTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTG  
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCTGATGCTGAAACCACTGCTGCT  
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG  
TAAAGACATTCCAGTTTACCCAAATGGGTGGGGATCTCCCGAATGGTAGAGTGTGTCCCT  
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACATTTCATGCTTCCTGTGATTTC  
ATCCAACTACTTACCTTGCCTACGATATCCCCTTTATCTCTAATCAGTTATTTTCTTTCAA  
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

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**FIGURE 282**

MKFLAVLVLLGVSI FLVSAQNPTTAAPADTYPATGPADDEAPDAETTAAATTATTAAPTAT  
TAASTTARKDIPVLPKWVGDLNGRVCP

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**FIGURE 283**

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGTTCCAACCTTGGACCC  
CTAGGGGTCTGGATTTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGAATGC  
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTACGGTGGCCTGGTCCCTCCTTGCCGAGAGA  
GTGTCTTGGGTCAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC  
ACTTGCCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG  
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGGCG  
GCAAACTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCCAGCTCCT  
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGTAAAAAAACCACAGGCTGG  
ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA  
CCCCAAAGAGCTTTCATTGTATCTATTGATTTTTACCACATTAGCAATTAAAACTGAGAAAT  
GGGCCGGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGTGGAT  
CACCTGAGATCAGGAGTTCAGACCAGCCTGGCCAAATGGTGAAACCTTGTCTACTAAAAA  
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCAGTTACTCGGAGGCTGAG  
GCAGGAAAATCGCTTGAACCCAGGAGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT  
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

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**FIGURE 284**

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGRAG  
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLCCWPVGVARGGALCQ

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GTCA**TCAG**CCAGTGCCTGCTCTGTGCTGCTCTGGGCCCTGGCAATGGTGACCCGGCTGCTCTCA  
GCGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCTGCTCTTCCATGG  
GACCTGCACTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGACGGCTGACAA  
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGCGAGGAGGTGAGC  
CGGGCCGGGATGCAGCCAGGAATTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA  
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCAGGCACAGA  
AGGTGCTACGGGACAGCGTGCAGCGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT  
GCCTACCGAGAATTGTAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC  
CCTCACAGGCCACGTGCAGCGGCAGAGCGGGAGATGGTGGCACAGCAGCATCGGTGCGAC  
AGATCCAGGAGAGACTCCACACAGCGGCGTCCAGCCT**CGA**ATCTGCCTGGATGGAATGAG  
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG  
CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCACTTCTGACACAGCAGACGAGACAGAC  
GCAGGCGGGGACAAAGGACAGGATGTAGCCCCATTGGGGGAGGGGTGGAGGAAGGACATGTA  
CCCTTTCATGCCTACACACCCCTCATTTAAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 286**

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLLFHGTLQLGQALNGVYRTTEGRLTK  
ARNSLGLYGRRTIELLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK  
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAAQQHRLRQ  
IQLRLHTAALPA

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**FIGURE 287**

GGCAAC**ATG**GCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAATTTGCAT  
 CCTGGTGATCACCTTACTCCTGGACCAGACCACCAGCCACACATCCAGATTAAAAAGCCAGGA  
 AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTGAAAAAGCTC  
 TGGACAGAAGTCAATGCCTTGAAGGAAATTCAGCCCTGCAGACAGTCTGTCTCCGAGGCAC  
 TAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCCATGAGGCCAATG  
 AAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAACCTCCGACGAAATCAACGCC  
 CTCCAAGACTATGGTAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA  
 CATGGTCACGGAAGGCAAGTTTGTGTACGTCAACGGAATCGCTATCTCCTTCCTCAACTGGG  
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAACTGTGTCTGTCTCCCAATCAGCTCAG  
 GGCAAGTGGAGTGATGAGCCCTGTCGAGCAGCAAGAGATACATATGCGAGTTTACCATCCC  
 TAA**ATAG**GTCTTTCTCCAATGTGTCTCCAAGCAAGATTTCATCATAACTTATAGGTTTCATGA  
 TCTCTAAGATCAAGTAAAAATCATAATTTTACTTATTAAAAAATGCAACACAAGATCAAT  
 GTCCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGGCCCT  
 TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCT  
 AAACAGACTAAAATCTTCTCTCTAGTCTTCTCACTTGTACAAACCCAGTTTGTTTTCAAA  
 AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT  
 TTCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATCCCTACATCAGAGACTCTAGGT  
 GCTATATAATCCAAAACTTTTCAGCCTGTTGCTCATTCTGTCCCATGCTGGCAATAATACC  
 TGTGCAGCCCATTACCCTTATTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTTGTCT  
 GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTGATTTTTTTTTTTTCTTCATGCC  
 TACCCTTTTTTTGGAAGTTTCCAGCCGCAATTGAAATGAAATGACAAGGTGTATATTGAT  
 CAATTTTCATTCCCACCATTGCATTACAACCTCTAACTTAAATGGGTAAACCTAAGGCATAT  
 CAAAGAAGCAGATTGCATGATAAACGGAATAGAAAAAAGAACCTACATTTATTTTGCTTT  
 AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCCCTTTTACATTT  
 TCGTATATTTATTTTTTTTAGCCATCATTATATGTTTAAAGTCTATTATGGGCAACCAATCTT  
 TGGAGCTGAAACTGAATTTAAAGAATGCTATCTTGGAAAATTGCATACGCTCTGTGCAATT  
 TTTTATTCTGCCTAGTGCTATTCTGCTTGTTTAACTAGATTGTACAAAATAAATTCATTGCT  
 TAATATCAAATTACAAAGTTTAGACTTGGAGGGAATGGGCTTTTTAGAAGCAACAATTTT  
 AAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATAT  
 CCCACTTTGCAAACTTAACTACACATGCTTGGAAATTAAGTTTTAGCTGTTTTTCATTGCTCA  
 ATAATAAAGCCTGAATTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 288**

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHKKRRVRDKDGLKTQIEKLWT  
EVNALKEIQALQTVCLRGTKVHKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ  
DYGKRS LPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSSQAQK  
WSDEACRSSKRYICEFTIPK

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**FIGURE 289**

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGAGGTTCCCCGCGCGC  
CCCCAGCCCCCGCGCC**ATGA**AGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCTGCA  
GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTCGCTGCGCTG  
GAGTCGGCGGCGGAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCCTCAACCCGCT  
GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT  
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG  
GCCCTGACAGTGTTTGGCT**TGA**GCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC  
CACCCGCGAGGGCTGAAAACCCCGCCGCGGGGAGGACCGTCCATCCCCTTCCCCGGGCCCT  
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAA

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**FIGURE 290**

MKLAALLGLCVALSCSSAAAFIVGSAKPVAQPVAALESAAEAGAGTLANPLGTINPLKLLLS  
SLGIPVNHLEGSQKCVaelGFPQAVGAVKALKALLGALTVEG

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**FIGURE 291**

TGAAGGACTTTTCCAGGACCCAAAGGCCACACACTGGAAGTCTTGACGTGAAGGGAGGCAC  
 CTTGGCCTCCGACGCCGATCACATGAAGGTGGTGCCAAGTCTCCTGCTCTCCGTCTCCTG  
 GCACAGGTGTGGTGGTACCCGGCTTGGCCCCAGTCCTCAGTCGCCAGAGACCCAGCCCC  
 TCAGAACGAGACCAGCAGGGTAGTGCAGGCTCCAGGGAGGAAGAGGAGATGAGCAGGAG  
 CCAGCGAGGAGAAGCGCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTT  
 GCCAAGGAGACTTCAAACCTCGGATTCAGCCTGCTGCGAAAGATCTCCATGAGGCACGATGG  
 CAACATGGTCTTCTCTCCATTGGCATGTCCTTGGCCATGACAGGCTTGATGCTGGGGGCCA  
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGGCTCCACTTGCAGGCCCTGAAGCCCACCAAG  
 CCCGGGCTCCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCCTCCTCCGCAACCTGGAAC  
 TGGCCTCTCACAGGGGAGTTTGGCCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCT  
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCCTGCTTATGAATTTTCGCAATGCCTCA  
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAAGAGACTCGGGGGAAAATCCCAAAC  
 GTTTGATGAGATTAATCTGAAACCAAATTAATTTCTGTGGATTACATCTGTTCAAAGGGA  
 AATGGTTGACCCCATTTGACCTGTCTTACCAGAGTCGACACTTTCCACCTGGACAGTAC  
 AAGACCATTAAAGGTGCCCATGATGTACGGTGACGGCAAGTTGCCTCCACCTTGACAAGAA  
 TTTTCGTTGTCATGTCCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCA  
 TGGAGAAAATGGGTGACCACCTCGCCCTTGAAGACTACCTGACCAAGAGACTTGGTGGAGACA  
 TGGCTCAGAAAACATGAAACCAGAAAACATGGAAGTTTCTTTCCGAAGTTCAAGCTAGATCA  
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCCACCCCTTG  
 CTGACCTTAGTGAATCTCAGCTACTGGAAGAAATCCTCAAGTATCCAGGGTTTTACGAAGA  
 ACAGTGATTGAAGTTGATGAAGGGGCACCTGAGGCAGTGGCAGGAATCTTGTGAGAAATTAC  
 TGCTTATTCATGCTCTCTGTCATCAAAGTGGACCGGCCATTTCAATTCATGATCATGAAG  
 AAACCTCTGGAATGCTTCTGTTCTGGCAGGGTGCTGAATCCGACTCTCCTATATTCAGG  
 ACATGCATAAGCACTTCGTGCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGA  
 TACCAGCAATGGATGGCAGGGGAGAGTGTTCCTTTTGTCTTAAGTATGTTAGGGTGTCTC  
 AAATAAATACAGTAGTCCCCACTTATCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGC  
 CTGAAACGGTGGACAGTGTCTGAACCTTATATATATTTTCTTACATACATACCTATGAT  
 AAAGTTTAAATTTATAAATTAGGCACAGTAAGAGATTAAACAATAAACAACATTAAAGTAAAA  
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA  
 CTAAGTGACTCATGGGCGAGGAGCATAGACAGTGTGGAGACATTGGGCAAGGGGAGAAATTA  
 CATCTGGGTGGACAGAGCAGGACGATGCAAGATTCATCCCACTACTCAGAATGGCATGC  
 TGCTTAAAGCTTTTATGATTGTTTATTTCTGGAATTTTCAATTTAATGTTTTGGACCATGGT  
 TGACCTGGTAACTGACATGCGAGAAAGCAAAACCATGGATAAGGGAGGACTACTACAAAA  
 GCATTAAATTTGATACATATTTTTTAAAAA

**FIGURE 292**

MKVVP S L L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E  
E E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I  
K R G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F  
D T E C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P  
V F T E V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L  
A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A  
T G R N L Q V S R V L R R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F  
L G R V V N P T L L

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**FIGURE 293**

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCAGACATGAG  
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG  
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG  
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTGTTCCC  
TGTCCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTGAGGGCAGGGGCCCCA  
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCCTGGGCCGTGTCCTGAGTCCC  
GAGCCCGACCATGACAGCCTGTACCACCCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC  
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA  
TCTACCACCCCCAGTAGGGCTCCAGGGGCCATCACTGCCCCCGCCCTGTCCAAGGCCAGG  
CTGTTGGGACTGGGACCCTCCCTACCTGCCCCAGTAGACAAATAAACCCAGCAGGCCAAA  
AAAAAAAAAAAAAAAAA

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**FIGURE 294**

MRLLLLVTSLVVVLLWEAGAVPAKVPPIKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL  
FPVQKPKLLTTEEKPRGQGRGFILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEE  
RPRWLWMPNHQVLLGPEEDQDHIYHPQ

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**FIGURE 295**

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG  
 TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGC  
 TGTTCCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA  
 TGGACCTGTTCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC  
 TAGTGCAATTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCT  
 GTGACATGACCTCTGGGGGTGGCGGTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATG  
 CGTGGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC  
 AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG  
 ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCAGCTG  
 CCCAATAAGTCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC  
 TGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT  
 ATGGAGAAGGAAAGTGTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGC  
 GACGCCCAGAAAACAGCATCTTATTACTCACCCTATGGCCAGCGGGAATTCAGTGCGGGATT  
 GTTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCAACGCCTTGTGTGCTGGAATGAGGG  
 TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTCCAGAGGCCAGT  
 CCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATATGGAACCTCATGTTGGTTA  
 CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTTTGTG  
 GGAGGGAACCCAGACCTCTCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTTACCCA  
 GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAATCATATTGACTCAAGAAAAAAA

MNQLSFLFLFIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN  
 GVIYQTFCDMTSGGGWTLVASVHENDMRGKCTVGRDWSQQGSKADYPEGDGNWANYNTFG  
 SAEATSDDYKNGPYDIPQAKDLGIWHVPNKSMPQHWNRSSLLRYRTDTGFLQTLGHNLFGI  
 YQKYPVKYEGEKCTDNGPVI PVVYDFGDAQKTASYSPYQGREFTAGFVQFRVFNNERAAAN  
 ALCAGMRVTGCNTEHHICIGGGYPFEASPPQCGDFSGFDWSGYGTHVGYSSSREITEAAVLL  
 FGR



**FIGURE 297**

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC  
 CACGAGGCTGCCGCATCTGCCCTCGGAACAATGGGACTCGGCGCGCAGGTGCTTGGGGCCG  
 CGCTGCTCCTGGGGACGCTGCAGGTGCTAGCGTCTGCTGGGGGCCGCCATGAAAGCGCAGCC  
 ATGGCGGCATCTGCAAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC  
 AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAACTTCCAACAGTACTGTGAAAC  
 CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG  
 GCATCTAATACAACAACACCAGGGATGGTCTCAACAATATGACTTCTACCACCTTAAAGTC  
 TACACCCAAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG  
 TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACATATGCAT  
 TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAC  
 GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTC  
 GGTATCGAACCATAGATGAACATGATGCCATCATTAAAGGAAATCCATGGACCAAGGATGGA  
 ATACAGATTGATGCTGCCTATCAATTAATTTTGGTTTATTAATAGTTTAAACAATATCTCT  
 CTTTTGAAAATAGTATAAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA  
 AAGATTCTTCAAGGTAACAAGGGTTTGGGTTTGAATAAACATCTGGATCTTATAGACCGT  
 TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAACAAGTCTATCTTTTTTTTTTGGCT  
 GGGGTGGGGGCATTGGTCACATATGACCAGTAATTGAAAGCGTCATCACTGAAAGACAGAA  
 TGCCATCTGGGCATACAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGT  
 AGCTCACATAAAGAAGTTTGTGTCAGAGCTGGATATATCTTAATTACTAATGCCACA  
 CAGAAATTATACAATCAAAGTATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTG  
 TGCTTTAAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

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**FIGURE 298**

MGLGARGAWAALLLGTQLVLLALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPSDH  
TNETSNSTVKPPTSVASDSSNTTVTMKPTAASNTTTPGMVSTNMTSTLKSTPKTTSVSQN  
TSQISTSTMVTHNSSVTSAASSVTITTTMHSEAKGSKFDTGSFVGGIVLTLGVLSILYIG  
CKMYYSRRGIRYRTIDEHDAII

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**FIGURE 299**

CAGCCGGGTCCTCCAAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGG  
 TCGCGGGGGGTCCTCGGGCTGTGGGACCGCTGGGGCCCCAGCCATGCGCAGCCCTGTGGGGAGGC  
 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCTGTGCCTGGCGCTTTCCTGTCTGCTGCTGGC  
 GCAGCTGTGAGACGCCGCAAGAATTTCGAGGATGTGAGATGTAAATGTATCTGCCCTCCCT  
 ATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCCTT  
 CATGTTGTGGAGCCCATGCCCTGTGCGGGGCGCTGATGTAGAAGCATACTGTCTACGCTGTGA  
 ATGCAAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCA  
 TTTTGGGCCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG  
 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT  
 TGCAATGCACACGATGTGCTAGCCCGCTCCCGAGTCGAGCCAACGTGCTGAACAAGGTAG  
 AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGG  
 CATGTTGTCTCCTCAGCTAAATTGGGAATTGAATCAAGGTGACTAGAAAGAAACAGGCAGACAA  
 CTGGAAGAAGTACTGAGTGGGTTTTGCTGGGTTTCAATTTTAATACCTTGTGATTTCACCAACT  
 GTTGCTGGAAGATTCAAACTGGAAGCAAAACTTGCTTGATTTTTTTTCTTGTTAACGTA  
 ATAATAGAGACATTTTTAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTATTTG  
 TGACTTTTACTAATAAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCTTTACCTGGAACA  
 AGCACTCTCTTTTTCACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTTG  
 TTGTTGTTGTTTTTTGTTTTGTTTTGTTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTT  
 AACCACTTTTTTCAAGTCACCTTTACTAAACAACTTTTTGTAATAGACCTTACCTTCTATTT  
 TCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAGAGCTGACTTACTCATTTG  
 ACTTTTGCACGTACTGTATTATCTGGGTATCTGCTGTGTCTGCACCTCATGGTAAACGGGAT  
 CTAAATATGCCTGGTGGCTTTTCAAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATG  
 CAATGCATCCTAGAACAACTGGCCATTGTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG  
 GTGTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT  
 TGCAATAAAGAAATTTTATTTTAAACCAAGCCTCCCTGGATTGATAATATATACACATTTG  
 TCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAAC  
 AGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATATTGGATAAAGTGGCTTTTT  
 CTTTCTATGTCTCTTTTGAATGTAACAATAAAAAATAATTTTGAACATCA

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**FIGURE 300**

MATLWGGLRLGSLLSLCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENS GHIYNKNIS  
QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIKVTII IYLSILGLLLLLYMVYLT  
L  
VEPILKRRLF GHAQLIQSDDDIGDHQPFANAHDVLARSRSRANVLNKVEYAAQQRWKLQVQEQ  
RKS VFDRHVVL S

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**FIGURE 301**

GCACCTGCGACCACCGTGAGCAGTC**ATG**GCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT  
CTGGGCTTGTCTGGCTCTGTGCTGCTGCTGCCAAGGCC**TT**CCTGTCCCGCGGAAGCGG  
CAGGAGCCGCCGCCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCA  
CCAGGCACCCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG  
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAGAGGTCTG  
ATGGGGCAGATTATTCCAATCTACGGTTTTTGGGATTTTTTATATATACTGTACATTCTATT  
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAAT**TGA**AAATCTAATATGGCGATAAAAA  
TCATTGTCTACATTAAACCTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA  
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCAAGTTTCACATAAGAATG  
TTTACTCAATGTTTAAGTGTGTTTGGCCCAAATTCACAATAACAAGGCAGAACTAGGACTT  
GAACATGGATCTTTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

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**FIGURE 302**

MAYSTVQRVALASGLVLALSLLLPAFLSRGKRQEPPTPEGKLGFRFPPMHHHQAPSDGQT  
PGARFQRSHLAFAKAKSGGGAGGGGSGRGLMGQIIPYGFIFLYILYILFKVSRIILI  
ILHQ

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CGGCTCGAGTGCAGCTGTGGGGAGATTTACAGGCATTGCCTCCCCTGGGTGCTCTTCATCT  
GGATTTGAAAGTTGAGAGCAGCATGTTTTGCCCACTGAAACTCATCTGCTGCCAGTGTTAC  
TGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTCCATGTG  
GGTGATTACAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATCAAGT  
AGACTGGACTCTGTCAACAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA  
ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGGTACACTTGATGGGGACATCTTATGC  
AATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACTATATCTGTGA  
AATCCGCCCTCAAGAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGGTACTGCATGTGCTTCCAG  
AGGAGCCCAAGAGCTCATGGTCCATGTGGGTGGATTGATTAGATGGGATGTGTTTTCCAG  
AGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAGGA  
GGAGATTGTATTTTCGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCCAGAGCTGGG  
GCCATTCTCGAAGATCGTGTGAACCTGGTGGGGACATTTTCGCAATGACGGTTCCATCGG  
CTTCAAGGAGTGGAGGAGTCAGATGAGGAGAACTACACTGCAATATCCACCTAGGGAACCT  
GGTGTTCAGAAAACCATTGTGCTGCATGTCAGCCCGGAAGAGCCTCGAACACTGGTGACCC  
CGGCAGCCCTGAGGCCCTCTGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTC  
TGTGCCACAATCTGTGCTCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGAAAATAA  
GAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACCGAAGAAGACTAATCCAGAGATAAAAG  
AAAAACCTGCCATTTTGAAAGATGTGAAGGGAGAAACACATTACTCCCCAATAATTGTA  
CGGGAGGTGATCGAGGAAGAAGAACCAAGTGA AAAATCAGAGGCCACTACATGACCATGCA  
CCCAGTTTGGCCTTCTCTGAGGTGAGATCGGAACAACCTCACTGAAAAAAAGTCAAGTGGGG  
GAATGCCAAAAACACAGCAAGCCTTTTGAGAAGAATGGAGAGTCCCTTCATCTCAGCAGCGG  
TGGAGACTCTCTCTGTGTGTCTCTGGGCCACTCTACCAAGTGATTTAGACTCCCGCTCTC  
CCAGCTGTCTCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG  
CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC  
TCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCGT  
GGATCAGACCCCTCTGTGGCGAGGTTCTTAGTGATGAGTTACTGGGAAGAATCAGAGATA  
AAAAACCAACCAATCAA

**FIGURE 304**

MFCPLKLILLPVLLDYSGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPG  
EHAKDEYVLYYYNSLSPVIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYYICEIRLKGES  
QVFKKAVVLHVLPEEPKELMVHVGGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY  
HKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCSIHLGNLVFKKTIV  
LHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLLPVLILIVKKTCGNKSSVNSTV  
LVKNTKKTNPEIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWPSLR  
SDRNNLEKKSGGMPKTQQAF

0000437 11501



**FIGURE 305**

CTATGAAGAAGCTTCTCTGAAAAACAATAAGCAAAGGAAAAACAATGTGTCCCATCTCACATG  
 GTTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG  
 AAACACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCC**ATG**CA  
 GGATGAAGATGGATACATCACCTTAAATATTAAACTCGGAAACCAGCTCTCGTCTCCGTTG  
 GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGG  
 ATGGTTGTGGGCTGGTGGCTCTGGGGATTTGGTCTGTCATGCAGCGCAATTACCTACAAGA  
 TGAGAATGAAAATCGCACAGGAACCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG  
 TAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCCTGTGACACAAAC  
 TGGAGATATTATGGAGATAGCTGCTATGGGTCTTCAGGCACAACCTAACATGGGAAGAGAG  
 TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG  
 AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT  
 GAGGCTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGTAGTTTTTGAAGA  
 TGAAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCTACCTTCTGTG  
 AGAACAAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT  
**TAA**TGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGT  
 ATGAATGCATCAGTAGCTGAAAAAAAAAAAAA

0090437 11501  
 1090437 11501

306/330

**FIGURE 306**

MQDEDGYITLNIKTRKPALVSVGPASSSWWRVMA LILLILCVGMVVGLVALGIWSVMQRNYL  
QDENENRTGTLQQLAKRFCQYVVKQSELKGT FKGHKCSPCDTNWRYYGDSYGFRRHNLWE  
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMF EFL  
EDGKGNMNCAYFHNGKMHPTFCENKHylmCERKAGMTKVDQLP

09900437.11501

CCACACGCGTCCGCGCAGTGCGCAGTTCTGCCTCCGCTGCCAGTCTCGCCCGCGATCCCGG  
CCCGGGGTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACC  
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCTCTCTTTGTGTAAGCCCGAGTGC GGAGAA  
GCCCGGGGCAAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTGC GCAGACAGCGGACAAGCAG  
CGGAGGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCGAGCAAAAGAAGCGGTGGTGGTGGG  
CGTCGTGGCCATGGCGCGGCTATCGCCAGCTCGCTCATCCGT CAGAAGAGGCAAGCCCGG  
AGCGCGAGAAATCCAACGCCTGCAAGTGTCTCAGCAGCCCCAGCAAAAGGCAAGACAGCTGC  
GACAAAACAAGTTAAATGTCTTTCCGGTGCCTCAACTCTTCGGCTCCAAGAAGAGCGCGAG  
AAGAAGACAGAGCTCAGCTTCAAGGGTAGTTACCAAGCTATACAGCCGACAAGGCTACC  
ACTTGACGCTGCAGGCGGATGGAACCATTGATGGCACC AAAGATGAGGACAGCACTTACACT  
CTGTTTAACTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT  
GTACTTGCAATGAACAGTGAGGGATACTTGTACACCTCGGAAC TTTTACACCTGAGTGCA  
AATTCAAAGAATCAGTGTTTGAAATATTATGTGACATATTATCAATGATATACCGTCAG  
CAGCAGTCAGGCCGAGGTTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA  
CCATGTGAAGAAGAACAAGCCTGCAGCTATTTTCTGCC TAAACCACTGAAAGTGCCATGT  
ACAAGGAGCCATCACTGCAGATCTCAGCGAGTTCTCCCGATCTGGAAGCGGGACCCCAAC  
AAGAGCAGAAGTGTCTCTGGCGTGTGAACGGAGGCAATCCATGAGCCACAATGAATCAAC  
GTAGCCAGTGAGGGCAAAAGGAAGGCTCTGTGAACGAACCTTACCTCCAGGTCTGTTGAAT  
TCTTCTAGCAGTCTCTACCCAAAGTTCAAATTTGTGAGTACATTACCAACAACCAAGCAG  
CCAGGTTCACTATTCTATCTGCCATTAGACCTTCTATCATCCCTACTATAAGC

**FIGURE 308**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498  
><subunit 1 of 1, 245 aa, 1 stop  
><MW: 27564, pI: 10.18, NX(S/T): 1  
MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGTSCDKNKLNVF SRVKLFGSKKRRRRRP  
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA  
MNSEGILYTSSELTPECKFKESVFENYYVTYSSMIYRQQSGRGWYLG LNKEGEIMKGNHVK  
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSM SHNEST

**N-glycosylation site.**

amino acids 242-246

**Glycosaminoglycan attachment site.**

amino acids 165-169, 218-222

**Tyrosine kinase phosphorylation site.**

amino acids 93-100

**N-myristoylation site.**

amino acids 87-93, 231-237

**ATP/GTP-binding site motif A (P-loop).**

amino acids 231-239

**HBGF/FGF family proteins**

amino acids 78-94, 102-153

**FIGURE 309**

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG  
 ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG  
 CAACCTGGATATTCTGAGACATATTTTGGGGGGATTTTCAGTGAAAAAAGTGGGGGATCCCC  
 CCATTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTTGGGTTCCCTCCTGACATTGGCAGTG  
 CCCAGTAGGGGTGGGATGAGCGAATATTTCCCAAAGCTAAAGTCCCACACCTGTAGATTAC  
 AAGAGTGGATTGTCAGGAGTGTGCCCCAAAATACAGTGAAAGGTGCCTGAAGATATTTAA  
 ACCACGTCCTTGAAATTTAGTGGGCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTG  
 GAGAGGAGGGAAAGGGGACGTTTTCAATAGGAGGCCAAACTCGAGGGTGGGATCCACTGAGG  
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCACGGGTGGTAAGTGGCTGCT  
 GTGGAGGGGGGTACGTGAGGGGGGGTCTGGGGCTTATCCTCAGGTCCTGTGGGTGGGGCAG  
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCAG  
 CGCGCTCCGGGCGCCTGCCGGTTTGGGGGTGTCTCCTCCCGGGCGCTATGCGCGGCGCTGGC  
 CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCGCGAGCCCGGGGCGACCGGCGCGGTGTCGG  
 CGCAGCGGCGCTGTGTCCCCCGGGCACCAGTCCCTTTGCCAGAAGCAGCTCCTCATCTCTG  
 CTGTCCAAGGTGCGACTGTGCGGGGGGGCGGCCCGCGCGGCCGAGCCGCGGCCCGAGCCTCA  
 GCTCAAAGGCATCGTCACCAAAGTGTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCG  
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAGCTCCTTCACCCACTTCAACCTGATCCCT  
 GTGGGCCTCCGTGTGGTCACCATCCAGAGCGCCAAAGCTGGGTCACTACATGGCCATGAATGC  
 TGAGGGACTGCTCTACAGTTTCGCCGATTTACAGCTGAGTGTGCGTTTAAAGGAGTGTGTCT  
 TTGAGAATTACTACGTCCTGTACGCCTCTGCTCTCTACCGCCAGCGTCGTTCTGGCCGGGCC  
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTCAATGAAGGAAACCGAGTTAAGAAGACAA  
 GGCAGCTGCCCACTTTCTGCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC  
 ACAGTGTCCCCGAGGCCTCCCCTTCCAGTCCCCCTGCCCCCTGAATGTAGTCCCTGGACTG  
 GAGGTTCCCTGCACTCCAGTGAGCCAGCCACCACCACAACCTGT

099047.44604

**FIGURE 310**

MAALASSLIQKREVREPGGSRPVSAQRVRCPRGTSKLCQKQLILLKSVRLCGGRPARPDR  
GPEPQLKGIVTKLFCRQGFYLOANPDGSIQGTPEDTSSFTFNLIPIVGLRVVTIQSAKLGHY  
MAMNAEGLLYSSPHFTAECRFKECVFENYVYLYASALYRQRSSGRAWYLGLDKEGQVMKGNR  
VKKTKAAAHFLPKLLEVAMYQEPSLSVPEASPPSPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

**FIGURE 311**

**ATG**GCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGCGCGGGAGCAGCACTG  
GGACCGGCCCTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACC GC GGGCTCTGCAACG  
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG  
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTCAGGCAAGGCTACTACTT  
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT  
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT  
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT  
TAAAGAATCTGTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG  
AATCTGGTAGAGCCTGGTTTTTGGGATTAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA  
GTAAAGAAAACCAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTGGCATGTACCG  
AGAACCATCTTTGCATGATGTTGGGGAAACGGTCCCAGGCCTGGGGTGACGCCAAGTAAAA  
GCACAAGTGCCTCTGCAATAATGAATGGAGGCAAACCAGTCAACAAGAGTAAGACAACA**TAG**

CGG0437.11504

**FIGURE 312**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWDPSASRRRSSPSKNRGLCNGNLVDIFS KVRIFGLKKRRRLR  
 RQDPQLKGIVTRLYCRQGYIQLMHPDGA LDGTDKDDSTNSTLFNLI PVGLRVVAIQGVKTGLY  
 IAMNGEGYLPSELFTPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR  
 VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKS KTT

**N-glycosylation site.**

amino acids 100-104, 242-246

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 28-32, 29-33

**Tyrosine kinase phosphorylation site.**

amino acids 199-207

**N-myristoylation site.**

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

**HBGF/FGF family proteins.**

amino acids 104-155, 171-198



**FIGURE 313**

GGGGAGAGGAATGACCATGTAAAGGAGACATTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCCTTGCAAAAAAT  
 GAAGGATGCAGGACGCGACTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA  
 ACGAAGCTTTTTTCTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGAGCAATCAAGAAATG  
 AAATAAACAGAGTTAGACCCGCGGGGGTGGTGTGTTCTGACATAAATAAATAATCTTAAGCAGCTGTTCCCT  
 CTCCCCACCCCCAAAAAAGGATGTTGGAATGAAGAACCGAGGATTCACAAAGAAAAAGATGTTCTATTT  
 TTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTTGAATGAAAAAGTTTGGGGCTTTTTTAGTAAAGTAA  
 AGAAGTGGTGGTGGTGGTCTTTCTTTCTTTTGAATTTCCCACAAGAGGAGAGGAATTAATAATACATCTGC  
 AAAGAAATTTCAGAGAAGAAAAGTTGACCGCGGAGATTGAGGCATTGATTGGGGGAGAGAAACCGAGAGAGCA  
 CAGTTGGATTGTGCCTATGTGTGACTAAAAATGACGGATAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTT  
 TTTTAAATTTTTATCTCTTTGGTATCAAGATCATGCGTTTTCTCTTGTCTTAACCACCTGGATTTCCATCT  
 GGATGTTGCTGTGATCAGTCTGAAATACAACTGTTGAATTCAGAAGGACCAACACAGATAAATATGAATG  
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGTCTTAGGTTTAAACAGGGCCCTATTGACCCCT  
 GCTTGTGGTGTCTGTGGCTCTTCAACTCTTGTGGTGGTGGTCTGTGGTGGGGCTCAGACCTGCCCTCTGTGT  
 GCTCTGCAGCAACAGTTTCAGCAAGGTGATTTGTGTGCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCC  
 ACCAACACAGCGCTGCTGAACCTCCATGAGAACCATAATCCAGATCATCAAGTGAACAGCTTCAAGCACTTGAG  
 GCACTTGGAAATCCTACAGTTGAGTAGGAACCATATCAGAACCATTGAATTTGGGGCTTTCAATGGCTGGCGA  
 ACCTCAACACTCTGGAACTCTTTGACAATCGTCTTACTACCATCCGAATGGAGCTTTGTATACTTGTCTAAA  
 CTGAAGGAGCTCTGGTTCGGAACAACCCCATTTGAAGCATCCCTTCTTATGCTTTTAAACAGAAATCCTTCTTT  
 GCGCGCATAGACTTAGGGGAATGAAAAGACTTTCATACATCTCAGAAGGTGCCCTTGAAGGCTCTGCCAAT  
 TGAGGTATTTGAACCTTGCCATGTGCAACCTTCGGGAATCCCTAACCTCACACCGCTCATAAACTAGATGAG  
 CTGGATCTTTCTGGGAATCATTTATCTGCCATCAGGCCTGGCTCTTCCAGGGTTGATGCACCTTCAAAAAT  
 GTGGATGATACAGTCCAGATCAAGTGATTGAACGGAATGCCCTTGACAACCTTCAGTCACTAGTGAGATCA  
 ACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACAT  
 TTACATCACACCTTGGAACTGTAACCTGTGACATACTGTGGCTCAGCTGGTGGATAAAGACATGGCCCCCTC  
 GAACACAGCTTGTGTGCCCGGTGTAACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGA  
 ATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCT  
 GAGCTGAAATGTGGGCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACA  
 TGGGGCGTACAAAGTACCGGTAGCTGTGCTCAGTGAGGTACGTTAAATTTACAAATGTAACCTGTGCAAGATA  
 CAGGCATGTACACATGTATGGTGAGTAATCCGTTGGGAATCTACTGCTTCAGCCACCCCTGAATGTTACTGCA  
 GCAACCACTACTCCTTTCTCTTACTTTCAACCGTCACAGTAGAGACTATGGAACCGCTCCTGAGATGAGGACG  
 GACCACAGATAACAATGTGGGTCCTCAGTGGTGCAGTGGGAGACCACCAATGTGACCACCTCTCTCACAC  
 CACAGAGCACAAGCTGCAGAGAAAACTTACCATCCAGTGACTGATATAACACTGGGATCCAGGGAAT  
 GATGAGTGCATGAAGACTACCAAAATCATCTATTGGGTGTTTTGTGGCCATCAACTCATGGCTGCAGTGATGCT  
 GGTCAATTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCAGCCCCAACAGGACTGTTGAAATTA  
 TTAATGTGGATGATGAGATTACGGGAGACACCCATGGAAAGCCACCTGCCATGCCCTGCTATCGAGCATGAG  
 CACCTAAATCACTATAAATCATCAAAATCTCCCTTCAACCACACAACAACAGTTAAACAAATAAATCAATACA  
 CAGTTTCAGTGACACCGCTTATTGATCCGAATGAACCTTAAAGACAATGTACAAGAGACTCAAAATCTAAACA  
 TTTACAGAGTTACAAAAAACAAACATCAAAAAAAGACAGTTTATTAAAAATGACACAATGACTGGGCTAA  
 ATCTACTGTTTCAAAAAGTGCTCTTACAAAAAACAAAAAGAAAGAAATTTATTTATTAATAATCTATTG  
 TGATCTAAAGCAGACAAAAA

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**FIGURE 314**

MLNKMTLHPQQIMIGPRFNRLFDPLLVLALLQLLVVAGLVRAQTCPSVSCSNQFSKVIC  
VRKNLREVPDGISTNTRLLNLHENQIQIIVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS  
YISEGAFEGLSNRLYNLAMLNCLREIPNLTPLIKLDLDELDSGNHLSAIRPGSFQGLMHLQKL  
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNDIL  
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE  
LKCRASLTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVDGTGMYTCMVSNSVGN  
TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTDNNVGPFPVVDWETTNVTTSLTPQ  
STRSTEKFTTIPVTDINSGIPGIDEVMKTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN  
HHAPTRTVEIINVDEITGDTPMESHLMPAIEHEHLNHYSYKSPFNHTTTVTNTINSIHSS  
VHEPLLIRMNSKDNVQETQI

**Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,  
434-438, 442-446, 488-492, 606-610

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537

0990137-11601

**FIGURE 315**

GCGCGGGGAGCCCATCTGCCCCAGGGGACGCGGGCGCGGGCCGCGCTCCCGCCCGGCACAT  
 GGCTGCAGCCACCTCGCGCGCACCAGGGCGCGCGCCAGCTCGCCGAGGTCCGTGCGA  
 GCGCGCCGGCGCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCGCGCTCCGGGGATC  
 GGGATGTCCTCCTCCTCTCTCTCTGCTAGTTTCTACTATGTTGGAACCTTGGGGACTCA  
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGC  
 TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCAGATAATGAAGGGAACCAAAA  
 GTGGTGATCACTTACTCCAGTCGTATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG  
 AGTGGCCTTTGCTTCCAATTTCTTGGCAGGAGATGCCTCCTTGCAGATTGAACCTCTGAAGC  
 CCAGTGATGAGGGCCGCTACACCTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCAT  
 GTCATCTTAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC  
 AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCAGAGGCCATTTGTGTATT  
 ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGCTCTGCCTCCCAATCTAGGATT  
 GACTACAACCACCTTGGACGAGTTCTGCTGCAGAATCTTACCATGTCTACTCTGGACTGTA  
 CCAGTGCACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAACTGTACAGT  
 ATGTACAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG  
 ATTTTCTCTTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAGAAAGATATGAGGAAGAAGA  
 GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCGCTCTTGTGAACCCAGCT  
 CCTTCTTCTCAGGCTCTCGGAGCTCAGCTCTGGTCTTCTCTCCACTCGCTCCACAGCAAT  
 AGTGCCTCAGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCAC  
 CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAAGTCCACCATG  
 CTAATCTGACCAAGCAGAAACCACACCCAGCATGATCCCGAGCCAGAGCAGAGCCTTCCAA  
 ACGGTCTGAATTACAATGGACTTGACTCCACGCTTTCTTAGGAGTCAGGGTCTTTGGACTC  
 TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA  
 GTGAGCATTGCACGGAACAGATTGAGATGAGCATTTTCTTATACAATAACCAACAGCAAA  
 AGGATGTAAGCTGATTCATCTGTAAAAGGCATCTTATTGTGCCTTAGACCAGAGTAAGGG  
 AAAGCAGGAGTCCAAATCTATTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAGGTG  
 AGGTGAATATACCTAAAACCTTTAATGTGGGATATTTGTATCAGTGCTTTGATTACAATT  
 TTCAAGAGGAAATGGGATGCTGTTTGTAAATTTCTATGCATTTCTGCAACCTATTGGATT  
 ATTAGTTATTGACAGAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC  
 TGAGCTAACCACTCTAAGAACTCCAAAAAGGAAACATGTGCTCTTCTATTCTGACTTAAC  
 TTCAATTTGTCATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGTTGGAGA  
 AGAGTGAAATGAGTTTCTCCCACTCTATACCTAATCTCACTATTGTATTGAGCCCAAAATAAC  
 TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTCCATCTTCTATGATTGT  
 ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCTCAAAT  
 CAGATGCCCTAAGGACTTTCTGCTAGATATTCTGGAAGGAGAAAAACAACATGTCATT  
 TATCAAGCTCTTAGAAGAATTTCTTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATT  
 CCCAACATACCATTATAGTCTCTTCTTCTGAGAAAAATGTGAACCAAGATTGCAAGACTGG  
 GTGGACTAGAAAGGGAGATTAGATCAGTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA  
 TGGTGCCAGGCCTGTAGGAAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC  
 ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

09900427.11601  
 109717.406601

**FIGURE 316**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419
```

```
><subunit 1 of 1, 373 aa, 1 stop
```

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYVGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV  
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYCKVKNSGRYVWSHV  
ILKVLVRPSKPKCELEGEELTEGSDLTLCQESSSGTEPIVYVYQRIKEKEGEDERLPPKSRID  
YNNHPRVLLQNLMTSYSGLYQCTAGNEAGKESCVRVRVTQVYQSIGMVAAGVTVIGAGALLI  
FLRWLLTIRRKDKERYEEERPNIEDEAPKARLVTPSSSSGSRSSRSSSTSTSTANS  
ASRORTLSTDAAPQGLATQAYSLVGEPRSEPKKVHHANLTKAETPSMIPSQSRAFQT

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

**FIGURE 317**

CGCGAGCGCGGGGAGCCTGGGACCAGGAGCGAGAGCGCGCTACCTGCAGCCGCCGCCACGGCACGGCAGCCAA  
 CCATGCGCGCTCTGCTGTGCTTCTGCTCTCTGTGCGGAGTAGTGATTTTCGCAGAGAGTTTGGATTACTCACTACT  
 CCTGAAGAGATGATTGAAAAAGCCAAAGGGGAACTGCCTATCTGCCATGCAAAATTTACGCTTAGTCCCGCAAGA  
 CCAGGGACCGCTGGACATCTGAGTGGCTGATATCACCAGCTGATATCAGAAGTGGATCAAGTGATTATTTTAT  
 ATTCTGGAGACAAAATTTATGATGACTACTATCCAGATCTGAAAGGCCGAGTACATTTACGAGTAATGATCTC  
 AAAAGCTGGTGATGCTCAATAAATTAACGAATTTACAACTGTGAGTATGTTGCTTAAAGCTTTCAGGTGGCAGATGTTACG  
 TTGATGATCTGAAGAAATTTGGAAGTGACTTTAAGATAAAATGTGAACCAAAAGAGGTTCACTTCCATTACAG  
 TATGAGTGGCAAAATTTCTGACTCAGAAAAATGCCACTTCATGGTTAGCAGAAATGACTTCATCTGTTAT  
 ATCTGTA AAAAATGCCCTCTCTGAGTACTCTGGGACATACAGCTGTACAGTCAGAAACAGAGTGGGCTCTGATC  
 AGTGCCTGTTGGCTCTAAAGCTTGTCCCTCCTTCAAAATAAGCTGGACTAATTCAGGAGCCCATTTATAGGAAT  
 TTGCTGTCTAGCGCTCATTTGGTCTTATCATCTTTTGTCTGCTGCTGTA AAAAGGCCAGAGAAAGAAAATATGAAA  
 GGAAGTTCATCAGATATCAGGGAAGATGTGCCACTTCCAAAGAGCCGTACGTCACATGCCAGAGCTACATCG  
 GCAGTAATCATTATCCTCGGGTCCATGTCTCCTTCCAAACATGGAAGGATATTCAGAGCTCAGTATAACCAA  
 GTACCAAGTGAAGACTTTGAACGCACTCTCAGAGTCCGACTCTCCCACTGCTAAGTTCAGTACCCCTTACAA  
 GACTGATGGAATTACAGTTGTA~~TAAA~~AATATGGACTACTGAAGAACTGAAATATTGATTATTTGACTTTATTTT  
 AGGCCTCTAGTAAAGACTTTAATGTTTTTAAAAAAGCACAGGCCAGAGATTAGAGCAGCTGTAAGAACAC  
 ATCTACTTTTATGCAATGGCATTAGACATGAAGTCAGATGTCAATGTCAAAATTAGTACGAGCCAAATCTTTGT  
 TAAAAAACCTATGTATAGTGACACTGATAGTTAAAGATGTTTTATATATTTTCAATAACTACCCTAACAA  
 ATTTTAACTTTTCATATGCATATTCTGATATGTGGCTTTTAGGAAAAGATGGTTAATAGTTGATTTTCAA  
 AGGAAATTTTAAAAATCTTACGTTCTGTTAATGTTTTTGTATTTAGTTAAATACATTGAAGGGAAATACCCG  
 TTCTTTCCCTTTTATGCACACACAGAAACACGCGTTGTCTGCTCAAACTATTTTATTTGCAACTACA  
 TGATTTACACAAATCTCTTAAACACACACATAAAATAGATTTCTGTATATAAATAACTTACATACGCTCCA  
 TAAAGTAAATTTCTAAAGGTGCTAGAACAAATCGTCCACTTCTACAGTGTTCTCGATCCAACAGAGTTGATGC  
 ACAATATATAAATACTCAAGTCCAATATTA AAACTTAGGCACTTGACTAACTTTAATAAAATTTCTCAAACTA  
 TATCAATATCTAAAGTGATATATTTTTTAAGAAAGATTATTCTCAATAACTTCTATAAAAAATAGTTTGATGG  
 TTTGGCCCTCTAAGTCTCACTACTATTAGTAGAAGCTTTTAACTTTTAAATGTGTAGTAGAGTTTATCTACCTT  
 TTTCTCAACATGACCCAAACACATCAAAAACGAAAGTTAGTGAGGTGCTAAACATGTGAGGATTATCCAGTGAT  
 TCCGCTCACAAATGCATTCCAGGAGGAGGTACCCATGTCACTGGAATTTGGGCGATATGGTTTATTTTTCTTCCC  
 TGATTTGGATAACCAAATGGAACAGGAGGAGGTAGTGATTTCTGATGGCCATTCCCTGCATACATTCTGGCTT  
 TTTTCTGGGCAAGGTTGCCACATTTGAAGAGGTGGAATATAAGTTCTGAAATCTGTAGGGAAGAGAACACAT  
 TAAGTTAATTCAAAGGAAAAATCATCATCTATGTTCCAGATTCTCATTAAGACAAAGTTACCCACAACACT  
 GAGATTCACATCTAAGTGACACTCCTATTGTGAGGTCTAAATACATTAAAAACCTCATGTGTAATAGCGGTATAA  
 CTGTATAACAGTGCACCAATGTTTTCTAAGTGCATAAAGAAATGAATAAATCAACACAGTACTTCTTAAACAA  
 CTCTCAACCAAAAAGACCAAAAGCTGAACGAATGGAAGCTTTGAAGGACATGCTTTGTTTCTGAGGCTGGTT  
 CCACAGCTGCTAAGCCAGGAGTCACTTGGAGGCTTTTAAATCAAAAACATTTGAGCTGGAGGCCATTTCTT  
 AGCAAACTAATGCAGAAACAGAAAATCACTACCCGATGTTCTCACTTATAAGTGGGAGGTATGATAGAAT  
 TATGAACACAAAGAGGAAACATAGACATTTGAGCTATTGTTGAGAGGAGGCTGGGAGAGAAAGGAGCA  
 GAAAGATAACTATTGAGTACTGCTTTCACACCTGGGTGATGAATAATATGTACAACTAACTCTGTGACACA  
 GTTTTACCTATGGAACAACTCTATGTTATCCCTAACTAAAAATAAAGTTAAAAAARAAAAAARAAAAA  
 AAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAA  
 AAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAA

CGCGAGCGCGGGGAGCCTGGGACCAGGAGCGAGAGCGCGCTACCTGCAGCCGCCGCCACGGCACGGCAGCCAA

**FIGURE 318**

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></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361
```

&gt;&lt;subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLCFVLLCGVVDARSLSITTPPEEMIEKAKGETAYLPCKFTLSPEDQGFLDIEWLISPA  
DNQKVDQVILILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK  
APGVANKKIHLVLVLPKPSGARCYVDGSEEIGSDFKICKPEKESLPLQYEWQKLSDSQKMP  
SWLAEMTSSVIVSKNASSEYSGTYSYTVNRVRNGDQCLLRNLRVNPPSNKAGLIAGAIIGTLL  
ALALIGLIIFCCRKKRREEKEYEKVHHDREDVPPKSTNSTARSYIGSNHSSLSGMSPSNM  
EGYSKTQNVQPSDEFPQSPITLPAKFYPKYTDGITV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

**Tyrosine kinase phosphorylation sites.**

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,  
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

**FIGURE 319**

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGA  
 ATGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACAGCTGCCTCCAGGCAGCCAGCC  
 CTC AAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGC  
 CAATTTAACACCAAGAAGAATTGAGGCTGCTGGGAGGAAGGCCAGGAGGAACACGAGACTG  
 AGAGATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCCTCTGCCCTC  
 CTTTGTCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCTGGGTTTTACCCCTG  
 CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGT  
 GAAGGGGGTTGTTCCCCAGAAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG  
 CTCAGGATAACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGAT  
 GCTGAGAGCTGTTACCTTGTCCACACCTGCTGGAGTTCTACTTGAAAACGTGTTTTCAAAAA  
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAAC  
 TTGTTCTCATCGTGTCACAACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC  
 AGTGCACACAGGCGGTTTTCTGTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC  
 TCTGACCAAAGCCCTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAAATCTACAAGC  
 TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTGTTCCCTGTGTCAATTC  
 AACAGTCTCCCTTCCATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATTC  
 TTGGCCAGGATTATGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG  
 GTGCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTTGTATTTATTACAACCTATTTT  
 AATTAATGTCAGTATTTCAACTGAAGTCTATTTATTTGTGAGACTGTAAGTTACATGAAG  
 CAGCAGAATATTGTGCCCCATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGCGAG  
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT  
 GTTAAAAAACAGAGAGGGATGCTTGGATGTAAAACCTGAACCTCAGAGCATGAAAAACACACT  
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGGTAAGGTGCATCTGTTTGAAGG  
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTTCATT  
 TCCCACCCACACTCGCCAGCTCACCCCATCATCCCTTTCCCTTGGTGCCCTCCCTTTTTTTTT  
 TATCCTAGTCATTCTTCCCTAATCTTCCACTGAGTGTCAAGCTGACCTTGCTGATGGTGAC  
 ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCCTGCTAATAAAAGACAACATAA  
 CTCCAAAAA

090047.11604  
 109111/200660

**FIGURE 320**

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></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002
```

&gt;&lt;subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRQLSWLTARFCPPLLATASQMOMVVLPCLGFTLLWSQVSGAQGQEFHFGPCQVK  
 GVPVQKLWEAFWAVKDTMQAQDNITSARLLQEQVELNVSDAESCYLVTLLFEYFKTVFKNH  
 HNRTEVTRLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL  
 TKALGEVDILLTWMQFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130



**FIGURE 321**

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTCCCTTTGGCTC  
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTCC  
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG  
ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAAGCCCTTA  
GATGTGTGCTGCGTGACCAAGAACCCTCCTGGCGTTCTACGTGGACAGGGTGTTCAGGATCA  
TCAGGAGCCAAACCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA  
TGCAGAAAACTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC  
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA  
ATCCCTGGGAGAGCTCGACGTCTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT  
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT  
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGACAGTGAAAGTCC  
CACTGGCTGGCCTCAGGCTGTCTTATCCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT  
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT  
CCCATCTAATTTATGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT  
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATCCATATTTACCTATGA

**FIGURE 322**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST  
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ  
RQCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

**Signal sequence:**

amino acids 1-18

**N-glycosylation sites.**

amino acids 56-60, 135-139

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 102-106

**N-myristoylation site.**

amino acids 24-30

**Actinin-type actin-binding domain signature 1.**

amino acids 159-169

00000437.11601

**FIGURE 323**

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG  
AACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT  
AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACCTGCACCTC  
GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATCGTGGGGGCCGCCT  
CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCA  
ATGCCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC  
AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGACCCCATCAGAC  
CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA  
TGAGCAGAAGATACTCTGCATGGATTTCAGAGGCAACATTTTTGGATCACACTATTCGAC  
CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACCTCTCC  
TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCTGCCAGGCATGAACC  
CACCCCGTACTCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCAGTTC AACACC  
CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGT  
GCTGAAGCCCCGGGCCCGGATGACCCCGGCCCGGCCCTCCTGTTACAGGAGCTCCCGAGCG  
CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTCGAGTGAAC  
ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGTCG  
CTGG

**FIGURE 324**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSSWGGLIHLYTATARNSYHLQIHKNGHVD  
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNIFGSHYFDPENCRFQHQTLENGY  
DVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQFLSRRNEIPLIHENTPIPRRHTRSAEDDSE  
RDPLNLVKPRARMTAPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNTHAGGTGPEGCRPFA  
KFI

**Important features of the protein:****Signal peptide:**

amino acids 1-24

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 175-179

**N-myristoylation site.**

amino acids 33-39, 100-106, 225-231, 229-235

**HBGF/FGF family proteins**

amino acids 73-124

**FIGURE 325**

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**  
 GGCTGTCTCTGGGGTCTGGCTCTGCCCTTTTCTTCTCTGCTGGGAGGTTGGGGTCTCTGG  
 GAGCTCTGCAGGCCCCAGCACCCGAGAGCAGACACTGCGATGACAACGGACGACACAGAAG  
 TGCCCGCTATGACTCTAGCACCGGGCCACGCCCTCTGGA~~AA~~ACTCAAACGCTGAGCGCTGAG  
 ACCTCTTCTAGGGCCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA  
 GAGAATTTCCCTGCAAGAGAGACCAGGAGTTTACAAAAACATCTCCCAACTTCATGGTGC  
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC  
 ACAGTTCAGACCATCACAGGCAGTGATCCCAGGAAGCCATCTTTGACACCTTTGCACCGA  
 TGACAGCTCTGAAGAGGCAAAGACACTCACAAATGGACATATTGACATTGGCTCACACCTCCA  
 CAGAAGCTAAGGGCCTGTCTCAGAGAGCAGTGCCCTCTCCGACGGCCCCATCCAGTCATC  
 ACCCGCTCAGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCATCCAGTCATCACCCC  
 GTCACGGGCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCATCCAGTCATCACCCCGTCAT  
 GGTCCCCGGGATCTGATGTCACTCTCTCGCTGAAGCCCTGGTGACTGTCA~~AA~~ACATCGAG  
 GTTATTAATTGCAGCATCACAGAAATAGAAACAACA~~AA~~CTTCCAGCATCCCTGGGGCCTCAGA  
 CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACAGCTCTGC  
 CTGACTCCACTGAAGCA~~AA~~ACCACACATCACTGAGGTACAGCCTCTGCCGAGACCTGTCC  
 ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCCACTAA  
 CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCCTCAGTGGAGCTCTGGTCA  
 CAGTTAGCAGGAATCCCTTGAAGAAACCTCAGCCCTCTCTGTTGAGACCAAGTTACGTC  
 AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGAGCAGTGGGCA~~AA~~ACA~~AA~~CTTC  
 CTTTGCTGGGAGCTCTGCTTCTCTACAGCCCTCGGAAGCCGCCCTCAAGAACTTACCCC  
 CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACAGCAGGACCTT  
 CTTCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA  
 GATCACAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCCAGACTGCCCGGAC  
 GAGGCCGACCACAGAC**GTGA**GTGCAGGTGAAATGGAGGTTCTCTCTCTGCGGTGAGTGTG  
 TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC  
 CGGGA~~AA~~CTCCACGCCACGCGCCTCACTTCCAGGTCTCCTTACTGCGTGTGAGGAGGGCTA  
 ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGTGCCCTTAGCCTG  
 GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG  
 AAGGGCAGCATGTCCAAGCCCTA~~AA~~CCCCAGATGTGGCAACAGGACCTCGCTCACATCCAC  
 CGGAGTGTATGTATGGGAGGGGCTTCACTGTTCAGAGGTGTCCTTGGACTCACCTTGG  
 CACATGTTCTGTGTTTCAGTAAAGAGAGACCTGATACCCATCTGTGTGCTTCCATCTGCA  
 TTAA~~AA~~TTCACTCAGTGTGGCCCA~~AAAA~~AAAA

**FIGURE 326**

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTL  
 ETSSRASTPAGPIPEAETRGAKRISPAETRSFTKTSNFMVLIATSVETSAASGSPEGAGM  
 TTVQTITGSDPEEAIFDTLCTDDSSEEAKTLTMDILTTLAHTSTEAKGLSSESSASSDGPHPV  
 ITPSRAESSASSDGPHPVITPSRAESSASSDGPHPVITPSWSPGSDVTLAEALVTVTNI  
 EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL  
 STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLGALVTVSRNPLEETSALSVETPSY  
 VKVSGAAPVSIEAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETPTMDIATKGFPTSRD  
 PLPSVPPTTTNSSRGTNSTLAKITTSAKTTMKPQQPRRLPGRGRPQT

**N-glycosylation sites:**

amino acids 252-256, 445-449, 451-455

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 84-90

**Casein kinase II phosphorylation sites.**

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,  
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,  
 404-408, 414-418, 431-435

**N-myristoylation sites.**

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-  
 320, 349-355, 386-392, 397-403, 449-455

**ATP/GTP-binding site motif A (P-loop).**

amino acids 385-393

09090437.11504

**FIGURE 327**

GCGGAGCATCCGCTGCGGTCCTCGCCGAGACCCCGCGGGATTCCGCGGTCTTCCCGCGG  
 GCGGAGCAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCCGGGGTCTCTCGAGCGCCA  
 GAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAACCTAAGACCAGAGGGGAGGATTAT  
 CCTTGACCTTTGAAGACCAAACTAACTGAAATTTAAATGTTCTTTCGGGGGAGAAGGGAG  
 CTTGACTTACACTTTGGTAATAATTTGCTTCTGACACTAAGGCTGTCTGCTAGTCAGAAAT  
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCTTGCATCCAGTCATCTCTTTCTAAGGGAATC  
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTTCTTGTCTTTCAAC  
 AAAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA  
 GACAACCCAACCTGCTACCTATTTTTCTGTCCCACGAGGAAGCCTGTCCATTGAAACACGCA  
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG  
 CCAAGAGTTACCCAGGAAGATTTCTCTTACATGGCCAATTTTCAACAGCAGTCACCTCCCC  
 TAGCCCATCATCACAGATTATTCAAAGCCACCGATATCTCATGGAGAGACACACTTTCT  
 CAGAAATTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA  
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTTCACAATTTTCTCTGATCAAGAAA  
 TAGCTCATCTGCTGCCTGAAAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTTCTCCA  
 CATACCACCTCGGCTACTTCAAAGCCCGCCACCTTCTACCCACCAATGCTTCAGTGACACC  
 TTCTGGGACTTCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAAACCATGTCACTTTCTC  
 AGCCTCCCACGACCTCATTTTCTACAGTTTTTACACGGGCTCGGCTACACTCCAAGCAATG  
 GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA  
 AACCATACCGTTTACAGAAATCTCCAACCTAACTTTGAACACAGGGAATGTGTATAACCCTA  
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTGGGAAGGT  
 AGGGAGGCCAGTCCAGGCAGTTCTCCAGGGCAGTGTTCAGAAATCAGTACGGCTTCC  
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTTCTGGTGATAGGCC  
 TCGTCTCTCTGGGTAGAAATCTTTCGGAATCACTCCGAGGAAACGTTACTCAAGACTGGAT  
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT  
 TAGTAACCAGAAGCCCAATGAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG  
 TATTTTGAAGACAGGAAAATGCCCTTCTGCTTTCTTTTTTTTTTGGAGACAGAGTCTT  
 GCTCTGTTGGCCAGGCTGGAGTGCAGTAGCAGATCTCGGCTCTCACCACCACTCCGTCTC  
 CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA  
 CCACACCTGGGTGATTTTTGTATTTTTAGTAGAGACGGGGTTTACCATTGTTGGTCAGGCTG  
 GTCTCAAACCTCTGACCTGATGATCCACCTCCTCGGCTCCCAAGGTGCTGGGATTACAGG  
 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGAAGAAGGAATGAAGTG  
 GGAACCAAAATTAGGTAATTTTGGGTAATCTGTCTCTAAATATTAGCTAAAAACAAAGCTCT  
 ATGTAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTTCACTGGCTTTTATGCAAA  
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTCTTGGTTCAGATAAAATCAAC  
 TGTTTTATCAATTTCTAATGGATTGCTTTTTTATATGGAATTCCTTTAAACCTTATT  
 CCAGATGTAGTTCTTCCAATTAATATTTGAATAAATCTTTTGTACTCAA

00990437 111601

**FIGURE 328**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410

><subunit 1 of 1, 431 aa, 1 stop

><MW: 46810, pI: 6.45, NX(S/T): 6

MFFGGEGSLTYTLVIIICFLTTLRLSASQNCCLKSLEDVVIDIQSSLSKGIRGNEPVYTSTQED  
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP  
SLTRNLPSQELPQEDSLHGGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF  
KMDEASQQLLAYKEKGHSQSSQFSSDQEIAHLFPENV SALPATVAVASPHHTSATPKPATLL  
PTNASVTPSGTSQPQLATTAPPVTTVTSPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP  
TDSKGSLETIPFTEISNLTNLNTGNVYNPTALSMNSVESSTMNKTASWEGREASPGSSSQGSV  
PENQYGLPFEKWLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRDYLINGIYVDI

**Signal sequence.**

amino acids 1-25

**Transmembrane domain.**

amino acids 384-405

**N-glycosylation sites.**

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 415-419

**Tyrosine kinase phosphorylation site.**

amino acids 50-57

**N-myristoylation sites.**

amino acids 4-10, 48-54, 315-321

000043-1100  
100000-100000



**FIGURE 329**

CTCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCTGCTATGGGGTTGCCGTCTGCT  
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT  
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT  
 GGGATCCTCTTCTCTCGTGTCTTGGCACCATCTATGCAGAAAGGAAGGCCAGGAGACAAT  
 GAAGGGCAGGGTGTCCATCCGTGACAGCGCCAGGAGCTCTCGCTCATTGTGACCCGTGTGA  
 ACCTACCCGTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG  
 TCTTTACTGATCTCTCTGTTCGTCTTCCAGGACCTGCTGTCTCCCTCCCTCTCTCCAC  
 CTTCCAGCCTCTGGCTACAACACGCTGCAGCCCAAGGCAAAAGCTCAGCAAAACCCAGCCCC  
 CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACAGCCAAGCAGGGGAAGACAGGG  
 GCTGAGGCCCTCCATTGCGAGGGACTTCCAGTACGGGCACGAAGGACTTCTCAGTACAC  
 AGGAACCTCTCTCACCAGCGACCTCTCTCTGTCAGGGAGCTCCCGCCCCCATGACAGC  
 TGGACTCCACCTCAGCAGAGGACACCACTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCCAGG  
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTCTGGTGTCTGCTGAGCCTTCTGTACAG  
 CGCAGGCCTGATCGCCTTCTCAGCCACCTGCTCTGTGGAGAAAGGCTCAACAGGCCA  
 CGGAGACACAGAGAACGAGAAGTTCTGGCTCTCAGCCTTGACTCGGAGGAAAAAGGAAGCC  
 CTTTCCAGGCCCTGAGGGGACGTGATCTCGATGCTCCCTCCACACATCTGAGGAGGA  
 GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCTGGCCAGGCCAGCAT  
 GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCCACCTCAGCCTCAGAG  
 TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCTCCCCAGGCTCTCTTTCGATGTTTCCA  
 GCCTGACCTAGAAGCGTTTGTACGCCCTGGAGCCAGAGCGGTGGCCTTGTCTTCCGGCTG  
 GAGACTGGGACCTCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCCTGA  
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC  
 CTCATGCCAGTGTGCGACCCCTGCCTTCTCCCACTCCAGACCACCCCTGTCTTCCCTCCC  
 TGGCGTCTCAGACTTAGTCCCACGGTCTCTGTCATCAGCTGGTGATGAAGAGGAGCATGCT  
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACTGCATCCAGCCTTCCAGGAAGCCT  
 GTGAAAAACGTGATTCTGGGCCCAACCAAGACCACCAAAACCATCTCTGGGCTTGTGTCAG  
 GACTCTGAATTCTAACAATGCCAGTGACTGTGCACTTGAGTTTGGGGCCAGTGGGCTG  
 ATGAACGCTCACACCCCTTACGCTTAGAGTCTGCATTTGGGCTGTGACGTCTCCACCTGCC  
 CAATAGATCTGCTCTGCTGCGACACAGATCCACGTGGGACTCCCTGAGGCCTGCTAAG  
 TCCAGGCCTTGGTCAGGTCAGGTGCACATTGCAGGATAAGCCAGGACCGGCACAGAAGTGG  
 TTGCCCTTNCATTGGCCCTCCCTGGNCCATGCCCTTCTGCCCTTGGAAAAATGATGAAGA  
 AAACCTTGGCTCCTTCTGTCTGAAAGGGTTACTTGCCTATGGGTCTGGTGGCTAGAGA  
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 GCACAACCTATTTTTTTTCTTTTCCATTATTATTGTTTTTAAGACAGAATCTCGTGTCT  
 GCTGCCCAGGCTGGAGTGCAGTGGCAGCATCTGCAAACTCCGCTCCTGGGTTCAAGTGATT  
 CTCTGCCTCAGCCTCCGAGTAGCTGGGATTACAGGCACGACCACCACCTGGCTAATT  
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGCCAGGCTGGCTTGAACCTGTAC  
 CTCAAATGAGCCTCCTGCTTCTAGTCTCCCAAAATGGCCGGATTACAGGCATGAGCCACTGTG  
 TCTGGCCCTATTTCTTTAAAGAGTGAATTAAGAGTTGTCAGTATGCAAACTTGGAAAG  
 ATGGAGGAGAAAAAGAAAGAAAGAAAAAATGTCAACCATAGCTCFCACAGACTATGATT  
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 TTTACAGAGCAATTTATCTTGATATACAACCTTTGTATCTCGCCTTTCCACCTTATCGTTCC  
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 GCTGCATAAAAA

**FIGURE 330**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

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 FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQKGTGAEAPPLPG  
 TSQYGHERTSQYTGTS PHPATSPPPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI  
 LAPVLVLLSLLSAAGLIAFC SHLLLWRKEAQQATETQRNEKFWLSRLTAE EKEAPSQAPEGD  
 VISMPLHTSEELGFSKFVSA

**Important features:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 248-269

**N-glycosylation site.**

amino acids 96-99

**Fibrinogen beta and gamma chains C-terminal domain.**

amino acids 104-113

**Ig like V-type domain:**

amino acids 13-128

0000137-11304  
 109117-1210660